STIC-Biotech/ChemLib

From: Sent: To: Subject: Chan, Christina

Monday, February 11, 2002 4:06 PM Davis, Minh-Tam; STIC-Biotech/ChemLib RE: Rush search request for 09/775693

Please rush. Thanks Chris

-----Original Message-----

Davis, Minh-Tam

Sent:

Monday, February 11, 2002 3:34 PM

To:

Chan, Christina

Subject:

Rush search request for 09/775693

Please search in commercial database and in issued patent files:

1) SEQ ID NO:1-and-a-polypeptide encoded by SEQ ID NO:1. Please check to see any of said polypeptide is the same as SEQ ID NO:7 or 8.

Thank you.
MINH TAM DAVIS
ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

Online time:



Other (specify):

		\(\tau\) \(\text{DOD}\(\text{OOCT}\(\text{A}\) \\ \(\text{A}\) \(\text{A}\)
	TYPE OF SEARCH:	VENDOR/COST(where applic.)
Searcher:	NA Sequences:	STN:
Phone:	AA Sequences:	DIALOG:
ocation:	Structures:	Questel/Orbit:
Date Picked Up:	Bibliographic:	DRLink:
Date Completed:	Litigation:	Lexis/Nexis:
Searcher Prep/Review:	Full text:	Sequence Sys.:
Clerical:	Patent Family:	WWW/Internet:

Other:

,			1
			!
			i
			•
			i
·			

						•	
HIC F	EPAR1	MENT	OF	~1	an e	=0	~
U.S. C		WELL.	0	W.	LL CU		٠.
	Date	ont and	T			~	

Requestor's		Serial Number:		, i	
Name:		.स. ता प्रकारणका वाद्यान क		**	- ::
Date:	Phone:		Art Unit:	ý.	_ :
Search Topic: Please write a detailed statement	of search topic. Describe specificall	y as possible th	ne subject matter to be search	ed. Define any	y

STAFF USE ONLY

	The second of the second	A STATE OF THE PARTY OF THE PAR		The second second		Company of the Compan
	ompleted: <u>62-13-</u>		Search Search	Site	Vendor	SCHOOL SECURITY OF THE PARTY OF
Search	er Belertyc	4994		STIC		ÏG
Termin	al time: 2d	<u></u>		CM-1		SIN
Elapse	d time:	<u> </u>	<u> بر د جود ا</u> المهاجي		**************************************	Dialog
CPU ti	mê:	<u> </u>	Type of			APS A DESCRIPTION OF
Total ti	me: 25	. <u>1964 - 1</u>	<u></u>	N.A. Sequence	:	Geninfo
	er of Searches:	<u> </u>	1. 1.1.14 <u>.4.4.4.4.</u>	A.A. Sequence	(a. 11. 1 <u>. 21. 4.2</u>	SDC
	er of Databases:		. 15. 18. <u> 15. 2. 2</u> .	Structure	da a a a da <u>azerta da</u>	DARC/Questel
				Bibliographic	: <u>- ' </u>	Other CGN
•					**	

OM of: US-09-775-693-1 to: A_Geneseq_1101:*

out_format : pfs

About: Results were produced by the Gencore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

Database: A_Geneseq_1101:*
Database sequences: 522463
Database length: 74073290
Database length: 74073290

search time (sec): 93.400000

search information block:

length: 1239 US-09-775-693-1 -WAIT -THREADS-1

```
/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM42071 + 128.50
/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM40759 + 128.50
/SIDS2/gcgdata/geneseq/geneseqp/AAA1903.DAT:AAR86978 + 128.50
/SIDS2/gcgdata/geneseq/geneseqp/AA1993.DAT:AAR41001 + 128.50
/SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAB40638 + 128.50
/SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAB40638 + 128.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAB57016
                                                                                                                       seq_documentation_block:
ID AAB57016 standard; protein; 442 AA.
                                                                                                                      AAB57016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; antiinfective; gynaecological; neuroprotective; cytostatic; nephrotropic; antiinfective; gynaecological; vulnerary; gastrointestinal; neural; immune; reproductive; renal; antibacterial; gene therapy; neural; immune; proliferative disorder; antibacterial; gene therapy; cardiovascular; proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate cancer antigen protein sequence SEQ ID NO:1594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200055174-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2000; 2000WO-US05988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-SEP-2000
                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1999; 99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
alignment_block:
US-09-775-693-1 x AAB57016
                                                                                                                                                                                                                                                                                           prostate cancer associated gene sequences, referred to as prostate prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of cancer antigens, useful for treatment, prevention, and diagnosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                      Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                          (ROSE/) ROSEN C
                              percent similarity:
                                                                                            Sequence 442 AA;
                                                                                                                   invention.
                                                                                                                                                                                                                                                                                                                                                    2000-587513/55.
                                                       Quality: 2123.00
                                                Ratio:
                                             5.178
99.515
                                              percent Identity: 99.272
                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200.64
189.79
181.00
181.00
178.29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.0018
0.0027
0.0038
0.0038
0.0038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182
490
1043
1093
```

9.1e-41 2.0e-34

.4e-13

.0e-09

.9e-06 5e-07 3e-06

.4e-10

L.6e-60 .1e-187

1.7e-05 2.1e-05 2.4e-05 4.1e-05 8.9e-05 0.0001

0.0003 0.0002 0.0004 0.0004 0.0008 0.0008 0.0010 0.0017 0.0017 0.0017

Page 2

us-09-775-693-1.rag

851 CCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900 281 PhemetTyrLeuAsnGluValAlaGlyLysHisGlyValGlyArgIleAs 297 751 TTCATGTACCTGAACGAAGTCGCGGGCCAAGCATGGCGTGGGCCGTATTGA 800 264 ysvalThrAsnvalLysAspGlyThrThrHisGlnThrSerLeuGluLeu 280 701 AGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTC 750 247 oAsnThrProAspIleLeucjuIleGluPheLysLysGlyValProValL 264 651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700 231 GinAlaProProGlyLeuTyrThrLysThrGlnAspProAlaLysAlaPr 247 601 CAAGCGCCTCCAGGTCTACACGAAGACCCAGGACCCAGGCCAAAGCCCC 650 214 snieuMetHisrieserTyrGluAlaGlyrleLeuGluAsnProLysAsn 230 551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAAC 600 197 sGlyIleProIleProValThrProLysAsnProTrpSerMetAspGluA 214 501 CGGGATTCCCATCCCGAGCACCCGTGGAGCATGGATGAGA 550 181 TyrasnargeheLysGlyargasnaspLeumetGluTyralarysGlnHi 197 451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500 164 erbeualaProGiniteLysValIlealaProTrpArgMetProGluPhe 180 401 CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450 147 yAlaThrGlyLysGlyAsnAspGlnValArgPheGluLeuSerCysTyrS 164 351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGGTCAGCTGCTACT 400 131 LysGlnValGluileAlaGlnArgGluGlyAlaLysTyrValSerHisGl 147 301 AAACAAGTGGAAATGGCCCAGCGGGGGGGGGGGGCCAAGTATGTGTCCCACGG 350 Align seg 1/1 to: AAB57016 from: 1 to: 442 97 uPheValGluGluPheIleTrpProAlaileGinSerSerAlaiceuTyrG 114 151 GCACTGAAGCTTGGGGCCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200 81 AlaieuLysLeuGlyAlaLysLysValbhelleGluAspValserArgGl 97 101 ATCTGGCCAACATTGGCCAGAAGGAAGGAAGTTCGAGGAAGCCAGGAAGAAG 150 64 yrleuAlaAsnīleGlyGlnLysGluAspPheGluGluAlaArglysLys 80 47 rSerCysIleLeuValTrpLeuLysGlucinclyTyrAspValIleAlaT 64 51 crcgrocarccrcgrgrggcrgaaggaacaaggcrargacgrcarrgccr 100

```
AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon the proteins are collectively known as colon cancer antigens have cytostatic activity and can be used in gene diagnosis and treatment of diseases associated with inappropriate p
                                                                                     Claim 11; Page 7623-7624; 9803pp; English.
                                                                                       Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:

D AAG75416 standard; Protein; 442 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAG75416
                                                                                                                                                       N-PSDB; AAH34821
                                                                                                                                                                           Ruben SM, Barash SC, Birse CE,
                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                             03-NOV-1999;
                                                                                                                                                                                                                                      29-SEP-1999;
                                                                                                                                                                                                                                                 28-SEP-2000; 2000WO-US26524.
                                                                                                                                                                                                                                                                             05-APR-2001.
                                                                                                                                                                                                                                                                                                WO200122920-A2.
                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                  Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                               Human colon cancer antigen protein SEQ ID NO:5180.
                                                                                                                                                                                                                                                                                                                                                                               03-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                               AAG75416;
                                                                                                                                                              2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             431 GluTyrHisArgLeuGlnSerLysValThrAlaLys 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1151 AGCCAACTGATGCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414 luProThrAspAlaThrGlyPheIleAsnIleAsnSerLeuArgLeuLys 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397 uSerLeuTyrAsnGluGluLeuValSerWetAsnValGlnGlyAspTyrG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 alArgHisCysTleAlaLysSerGlnGluArgValGluGlyLysValGin 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     951 TGCTGAGCTGGTGTATACCGGTTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 ThrMetAspArgGluValArgLySIIeLySGlnGlyLeuGlyLeuLySBh 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 hrProAlaGlyThrTleLeuTyrHisAlaHisLeuAspIleGluAlaPhe 330
                                                                                                                                                                                                                     990S-0163280.
                                                                                                                                                                                                                                  99us-0157137
                                                                                                                                                                      Rosen CA;
```

Page 3

```
888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-775-693-1 x AAG75416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    percent Similarity: 99.515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAG75416 from: 1 to: 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of p by expressing in a patient's genome that affect the activity of p by expressing the inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. Additionally, N may be used to produce the colon cancer decided ps. By inserting the nucleic acids into a host cell and culturing the cell by inserting the nucleic acids into a host cell and culturing diagnosis to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37796 to AAH37204 and treatment of present sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention.
N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 442 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 GCACTGAAGCTTGGGGCCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                   301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                          114 luaspargTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
                                                                                                                                                                                                                                                                        351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 uphevalGluGlupheileTrpProAlaIleGlnSerSerAlaLeuTyrG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspValSerArgGl 97
                                                                                                                                                                                                  401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                             181 TyrAsnArgPheLysGlyArgAsnAspLeuMetGluTyrAlaLysGlnHi 197
                                                                                                                                                                 451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                        197
                                                                                        501 CGGGATTCCCCATCCCGGTCACTCCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 2123.00
                  ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAAC 600
                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 99.272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
```

```
seq_documentation_block:
                                                                                                                                                                                                      seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAG82054
                                   XX DEXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 CAAGCGCCTCCAAGGTCTCTACACGAAGACCCAGGACCCAAGCCAAAGCCCC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 snLeuMetHisIleSerTyrGluAlaGlyIleLeuGluAsnProLysAsn 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             701 AGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              851 CCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 pIleValGluAsnArgPhelleGlyMetLysSerArgGlyIleTyrGluT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                   1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 ThrMetAspArgGluValArgLysIleLysGlnGlyLeuGlyLeuLysPh 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 hrProAlaGlyThrileLeuTyrHisAlaHisLeuAspIleGluAlaPhe 330
                                                                                                                                                                                                                                                                                                                                                                 1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        951 TGCTGAGCTGGTGTATACCGGTTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                             1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                          364 alargHisCysTieAlaLysSerGlnGluArgValGluGlyLysValGln 380
                                                                                                                                                                                                                                                          1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                        S, epidermidis open reading frame protein sequence SEQ ID NO:1202.
                                                                                                                                                                    AAG82054 standard; Protein; 367 AA
                                                             Staphylococcus epidermidis SR1 strain; infection; diagnosis;
                                                                                                                   03-SEP-2001
                                                                                                                                            AAG82054;
                      staphylococcus epidermidis
                                                vaccination; endocarditis.
WO200134809-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
```

17-MAY-2001

09-NOV-1999;

09-NOV-2000; 2000WO-US30782.

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides C(II), given in AAG8H454 to AAG83120, from Staphylococcus epidermidis. CC (I) and (II) can have antibacterial activity and therefore can be used containing them which are used to produce the production of vectors (I) was containing them which are used to produce hosts cells which express the CC polypeptides. The polypeptides (II) via the production of vectors (II) cand/or nucleic acids) may then be contained the polypeptides (II) cand/or nucleic acids) may then be considered to vaccinate subjects and to raise antibodies against the bacteria. CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to CC AAH55090 represent specifically claimed S. epidermidis genomic DNA (I) the exemplification of the present invention. AAH55091 to CC AAH5509B represent oligonucleotide sequences and primers which are used constitution of the present invention. AAH55091 to CC N.B. The present intention specifically claims all the polynucleotide sequence listing of the present specification, consequences given in the sequence listing of the present specification, consequences are given in the disclosure for SEQ ID NO:4454 so even consequences are present for SEQ ID NO:4455 to 4462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAG82054 from: 1 to: 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                260 ACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                         160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGAGTTTTGTGGA 209
                                                                                           210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                 110 ACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·09-775-693-1 x AAG82054
                                                   68 pAspTyrValSerTyrAlaIleLysGlyAsnLeuMetTyrGluAsnAlaT 85
                                                                                                                                52 MetGlyAlavalGluCysHisIleIleAspAlaThrLysGluPheSerAs 68
                                                                                                                                                                                                           35 spValGiyGluGlyLysAspLeuAspValValTyrGlnLysAlaLeuAsp 51
                                                                                                                                                                                                                                                                                      18 aValGlnTrpLeuIleAspLysGlyTyrAspValValAlaCysCysLeuA 35
                                                                                                                                                                                                                                                                                                                           60 CCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCA 109
                                                                                                                                                                                                                                                                                                                                                                                                      10 AAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCAT 59
                                                                                                                                                                                                                                                                                                                                                                 2 LysaspLys1leValLeualaTyrSerGlyGlyLeuaspThrSerValal 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 345; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAH52904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-316495/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kimmerly WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367 AA;
            ......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          747.00
2.756
72.654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9905-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 40.214
Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373
```

```
1110 CAATGAGGAGCTGGTGAGC 1128
                                                                                                       1060 CTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTA 1109
358 raspGluLysLeuAlaThr 364
                                                                                                                                                                                        1010 GCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAGGTGTCCCGTC 1059
                                                               342 PheLysGlyAsnAlaTleValAsnGlyArgGlnSerProTyrThrLeuTy 358
                                                                                                                                              325 herieAspSerThröinGlnTyrVaiGluGlyAspVaiArgIleLysLeu 341
                                                                                                                                                                                                                              308 nIleTyrAsnGlyLeuTrpPheSerProLeuThrAspSerLeuLysLeup 325
                                                                                                                                                                                                                                                                     960 GGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACT 1009
                                                                                                                                                                                                                                                                                                             292 LysaspValalaHisPheLysProValIleGluLysGlnPheSerGluG1 308
                                                                                                                                                                                                                                                                                                                                                    910 CGGGAAGTGCGCAAAATCAAACAAGGCCTTGGGCTTGAAATTTGCTGAGCT 959
                                                                                                                                                                                                                                                                                                                                                                                            275 laGluValIleLeuLysAlaHisLysAlaLeuGluThrIleThrLeuThr 291
                                                                                                                                                                                                                                                                                                                                                                                                                                    860 GCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGAC 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   810 GAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAG 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 LeuAsnGlnLeuAlaGlyLysHisGlyIleGlyArgileAspHisValGl 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              760 CTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 .....AspGlyLysAspTyrGlnLeuAsp...AspLeuIleLeuTyr 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               710 ACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTCATGTAC 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    660 TGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 GluaspalaPheAspLeuThrThrProLeuGluGluThrProAspAsnal 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         610 CCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 lyArgAlaAsnGluCysGlyTleLeuGluAspProTyrAlaAlaProPro 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        560 ACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 oValSerIleAsnTyrAspSerProTyrSerIleAspGlnAsnLeuTrpG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     510 CATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 ......SerArgGluGluGluIleAspTyrAlaIleLysHlsAsnIlePr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 roLysLeuLysAlaPheAlaProValArgGluTrpAlaTrp...... 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 yLysGlyAsnAspGlnValArgPheGluValAlaIleLysAlaLeuAsnP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 GluileAlaGluLysThrAsnSerIleGlyIleAlaHisGlyCysThrGl 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 GAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 yrProLeuValSerAlaLeuSerArgProLeuIleAlaLysLysLeuVal 101
```

seq_documentation_block; seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAG91292

```
alignment_scores:
                                                                                                                                                                                                                alignment_block:
                                                                                                                                                                                                                                                    Quality: 619.50
Ratio: 2.261
Percent Similarity: 66.344
                                                                                                                                                       Align seg 1/1 to: AAG91292 from: 1 to: 401
                                                                                                                                                                                             US-09-775-693-1 x AAG91292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG91292 standard; Protein; 401 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C glutamicum protein fragment SEQ ID NO: 5046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a area useful for identifying the mutation point of a gene derived from a gene derived analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the exemple of the control of the printed specification, but was obtained in electronic format directly from the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAH66511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; SEQ ID NO: 5046; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                       Sequence 401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           European Patent Office.
                                     69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                               19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
21 rLeuLysLysMetIleAspGlyGluValIleAlaValSerLeuAspLeuG 38
                                                                         5 IleValLeuAlaTyrSerGlyGlyLeuAspThrThrValAlaIleProTy 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mizoguchi H, Ando S, Hayashi M, Ochiai K,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                              Gaps: 8
Percent Identity: 35.351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yokoi H;
```

```
116 GCCAG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 ATCGCCCAGCGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 TCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 lyGlnGlyGlyGluAsnMetAspAsnValArgGlnArgAlaLeuAspAla 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 AlaGlyLysGlnPheAsnGlyThrHisValAlaHisGlyCysThrGlyLy 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 snLeuGluIleIleAlaProAlaArgAspPheAlaTrpThr........ 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 AGATAAAGGTCATTGCTCCC.....TGGAGGATGCCTGAA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 sGlyAsnAspGlnValArgPheGluValGlyPheMetAspThrAspProA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 uTyrCysLeuproThrIleLysAlaAsnGlyMetTyrMetLysGlnTyrP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448 TTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 uAsnAsnValProTleGluGlnSerValLysSerProPheSerTleAspG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 roLeuValSerAlaIleSerArgProLeuIleValLysHisLeuValGlu 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 lnAsnValTrpGlyArgAlaIleGluThrGlyTyrLeuGluAspLeuTrp 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                548 AGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAG 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 ACACGGGATTCCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATG 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 AsnalaProThrLysAspIleTyrAlaTyrThrGluAspProAlaLeuGl 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       598 AACCAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGC 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 y...AsnAlaProAspGluVallleIleSerPheGluGlyGlyLysProV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              648 CCCCAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTG 697
                                                                                                                                                                                                                                                                                                                                                                                                             748 CTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTAT 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 alSerIle.....AspGlyArgPro...ValSerValLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     698 TGAAGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAG 747
                                                                                                                                                                                                                                                                                                                                                                   798 TGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACG 847
                                                                                                                                                                                                                                                                          848 AGACCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCC 897
                                                                                                                                                                                                                                                                                                                    255 uAspMetValGluAspArgLeuValGlyIleLysSerArgGluIleTyrG 272
                                                                                                                                                                                 898 TTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAA 947
                                                                                                                                                                                                                              272 luAlaProGlyAlaIleAlaLeuIleLysAlaHisGluAlaLeuGluAsp
998 TTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTG 1047
                                            948 ATTTGCTGAGCTGCTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAAT 997
                                                                                                                                     289 ValThrīleGluargGluLeuAlaArgTyrLysArgGlyValAspAlaAr 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....ArgAspLysAlaIleAlaPheAlaGluGl 161
```

```
seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAB79801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                     08-JUL-1999
08-JUL-1999
08-JUL-1999
08-JUL-1999
08-JUL-1999
08-JUL-1999
08-JUL-1999
08-JUL-1999
08-JUL-1999
                                                                                              09-JUL-1999;
09-JUL-1999;
                                                                                                                                                                                                                            08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUN-2000; 2000WO-IB00923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04~JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; unsaturated fatty acid; organic acid; unsaturated fatty acid; organic, organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200100843-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1198 AAGGAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1148 ATGAGCCAACTGATGCCACCGGGTTCATCAACATCAACTTCCCTCAGGCTG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum MP protein sequence SEQ ID NO:336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1098 ACTGTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATT 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB79801 standard; Protein; 401 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 .....HisGlyLeuSerSerLysIleAlaAsnLys 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1048 CAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCC 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372 heaspGlnThrLeuAlaLysGlyPheValGlnLeu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 rHisSerLeuTyrAspPheAsnLeuAlaThrTyrAspThrGlyAspThrP 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 ArgMetValLeuHisAlaGlySerIleThrileAsnGlyArgArgSerSe 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::: ||| ::::::||||||:::||| ||| :::
322 erLeuAspAlapheIleAspSerThrGlnGluHisValThrGlyAspIle 338
                                                          99DE-1031634
99DE-1031636
99DE-1032125
99DE-1032126
99DE-1032130
                                                                                                                                                                                                                                                                                                                                                                          99DE-1031435.
99DE-1031443.
99DE-1031453.
99DE-1031457.
                                                                                                                                                                                             99DE-1031592.
99DE-1031632.
                                                                                                                                                                                                                                               99DE-1031573.
                                                                                                                                                                                                                                                                        99DE-1031510.
99DE-1031541.
                                                                                                                                                                                                                                                                                                                     99DE-1031478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99DE-1031428.
99DE-1031434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0141031
```

1

```
alignment_block:
US-09-775-693-1 x AAB79801
                                                                                                                                                                                                                                          alignment_scores:
                                                                                               Align seg 1/1. to: AAB79801 from: 1 to: 401
                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR
PR
PR
PR
PR
PR
PR
PR
PR
                                                                                                                                                                                                                                                         AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum in microcorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic
21 rLeuLysLysMetIleAspGlyGluValIleAlaValSerLeuAspLeuG
                     69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                    19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                   compounds, vitamins, cofactors, polyketides and enzymes
                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 656-657; 1737pp; English.
                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases
                                              5 IleValLeuAlaTyrSerGlyGlyLeuAspThrThrValAlaIleProTy 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-137957/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-2000; 2000US-0187970
                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF71920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pompejus M, Kroeger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUL-1999;
09-JUL-1999;
09-JUL-1999;
14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUL-1999;
                                                                                                                                                                                         Quality:
                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                      401 AA;
                                                                                                                                                               619.50
2.261
66.344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99DE-1042124
99DE-1042129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99DE-1040765.
99DE-1040766.
99DE-1040832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99DE-1033006.
99US-0148613.
99DE-1040764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99DE-1042087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99DE-1041380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99DE-1033005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99DE-1032228
99DE-1032229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽,
                                                                                                                                                         Percent Identity: 35.351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schroeder H,
                                                                                                                                                                     Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haberhauer G;
 38
                                                                                                                                                                                                                                                                                                          glutamicum
```

f.,

```
116 GCCAG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 AlaGlyLysGlnPheAsnGlyThrHisvalAlaHisGlyCysThrGlyLy 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 TOCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 ATCGCCCAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 GlyAlaAlaGluSerIleValValAspAlaLysAspGluPheAlaGluGl 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 lyGlnGlyGlyGluAsnMetAspAsnValArgGlnArgAlaLeuAspAla 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 snLeuGluIleIleAlaProAlaArgAspPheAlaTrpThr....... 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      413 AGATAAAGGTCATTGCTCCC.....TGGAGGATGCCTGAA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 .....ArgAspLysAlaIleAlaPheAlaGluGl 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          448 TTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 roLeuValSerAlaIleSerArgProLeuIleValLysHisLeuValGlu 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            498 ACACGGGATTCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCATGGATG 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 lnAsnValTrpGlyArgAlaIleGluThrGlyTyrLeuGluAspLeuTrp 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                548 AGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAG 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     698 TGAAGGTGACCAACGTCAAGGATGGCACCCACCAGCCAGACCTCCTTGGAG 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             648 CCCCAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTG 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 AsnAlaProThrLysAspIleTyrAlaTyrThrGluAspProAlaLeuGl 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            598 AACCAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGC 647
                                                                                                                                                                                                                                                                                                ::: |||||||::: ||||||| :::|||||||||||:::
239 AlaileGluGluLeuAsnArgArgAlaGlyAlaGlnGlyValGlyArgLe 255
                                                                                                                                                                                                                                                                                                                                                                                                                               748 CTCTTCATGTACCTGAACGAAGTCGCGGGCCAAGCATGGCGTGGGCCGTAT 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 alSerIle.....AspGlyArgPro...ValSerValLeuGln 238
                                                                                                                                                                                                                                                          848 AGACCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCC 897
                                                                                                                                                                                                                                                                                                                                              798 TGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACG 847
                                                                                                                                                                       898 TTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTTGGACTTGAA 947
                                                                                                                                                                                                                 272 lualaproGlyalaIlealaLeuIleLysalaHisGlualaLeuGluasp 288
998 TTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTG 1047
                                         305 gTrpAlaGluGluValTyrAspGlyLeuTrpPheGlyProLeuLysArgS 322
                                                                                 948 ATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAAT 997
                                                                                                                           289 valThrIleGluArgGluLeuAlaArgTyrLysArgGlyValAspAlaAr 305
```

```
seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAG08821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1098 ACTGTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATT 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1048 CAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCC 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1148 ATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 erLeuAspAlaPheIleAspSerThrGlnGluHisValThrGlyAspIle 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1198 AAGGAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 ArgMetValLeuHisAlaGlySerIleThrIleAsnGlyArgArgSerSe 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 rHisserLeuTyrAspPheAsnLeuAlaThrTyrAspThrGlyAspThrP 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 ..........HisGlyLeuSerSerLysIleAlaAsnLys 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG08821 standard; Protein; 302 AA
                                                                                                                                                                                                                                                                                     09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                          protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 6508.
                                                                                                                                                                                                                                                     29-MAR-1999;
01-APR-1999;
06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2000 (first entry)
                                                                                                                                                                                   08-APR-1999;
16-APR-1999;
19-APR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
                                                                                               04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
                                                                                                                                                     28-APR-1999;
30-APR-1999;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                      25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                25-FEB-1999;
                                                      14-MAY-1999;
14-MAY-1999;
                                                      99US-0132048
99US-0132407
99US-0132484
99US-0132485
99US-0132487
99US-0132487
99US-0132863
99US-0134218
99US-0134218
99US-0134218
99US-0134219
                                                                                                                                                                              99US-0130510.
99US-0130891.
99US-0131449.
                                                                                                                                                                                                                                                                                          99US-0125788.
99US-0126264.
                                                                                                                                                                                                                                                                                                               9908-0123548
                                                                                                                                                                                                                        99US-0130077
                                                                                                                                                                                                                                     99US-0129845.
                                                                                                                                                                                                                                                99US-0128714
                                                                                                                                                                                                                                                         9905-0128234
                                    99US-0134370
99US-0134768
     99US-0135353
```

00000	NNNN	PR 2 PR 2	~ ~ ×	V 20 20	20 20 3	x0 x0 5	ਹਿਲ	ಶಸಶಸ	' ਸ਼ੱਸ਼ੋ	žπ	ਸ਼ੁੱਸ਼ ;	ž ž ž	7 R R	PR	PR PR	PR	PR	PR	PR	PR	PR	PR	PR	PR	PR	PR	PR	PR	PR	PR
27-JUL-1999; 9 27-JUL-1999; 9 28-JUL-1999; 9 02-AUG-1999; 9 02-AUG-1999; 9	3-JU 3-JU 3-JU 7-JU	3-JU	22-Ju	21-ji 21-ji	20-JI	19-J	19-J 19-J	19-J 19-J	16-J	14 - J	13-0	- 80	01-	30-	28-	23-	22-	18-	18.	18.	18	18 18	18 18	17 18	16	114	10	0 0	200	22.5
G-19)[-1][-1	F-1	121	E-1	1111	155	ar-	-10T-	dr.	ַבְּרָּיִבְּ	144	-10F-	JUN-	JUN-	NOC	NOL	NOC	JUN.	YOU.	-JUN	ADE-	ADC-	ADD-	-301	70	- Ju	10	-19	8-MA
999;	999; 999; 999;	999; 999; 999;	999	999	666 666 666	6661 6661	1999	1999 1999	1999 1999	1999	1999	199	199	-199 -199	-199 -199	-199 -199	-199 -199	-199	-199	-199	1-19 1-19	1-19 1-19	√-19 √-19	N-19 N-19	N-19	N-19	N-19	Z-10	N - 1 - 1	Y-1
10.10.10.10.10.1				•• •• •								,, ,,	9,	99,	9 00 0	000	999	9,00	99,	99	99;	99;	99;	99;	99;	,666	,666	,666	,666 ,666	666
990S-0145918. 990S-0145919. 990S-0145951. 990S-0146386. 990S-0146388.	9908 8066 8066	3066 3066 3066	3066 3066 3066	3066	1066 1066	066 066	066 066	990 066	066 066	166	991	991	991	999	99	999	9 9 9	9 9 9	9 9 9	999	و و	و و	9 9	9 9	و و	99	vo vo		21010	
-014 -014 -014 -014	-01	0100	3-01 -01	S-01	s-01 s-01	S-01 S-01	S-01	S-01	S-0	IS-0	0-SI 0-SI	JS-0	US-0	05-0 08-0	- Sn	-SOS-	US-	SOC -	-Sne	-806	-806	90S-	9US-	9US-	9US-	9US	S06(908	Snee	Suce
591 591 595 638	1521 1522 1527	4508 4519 4514	4508	4481	443	443	443	1443	1440	1436	1429	142: 1428	142	141	140	140	0139	0139	0139	0139	0139	013	013	013	013	-013 -013	-013 -013	-013	-013	-013
25,7686		v v v	7.5.8	6	32.	35.	32.	25.	20 00 0	24.	20.	390.	154.	991. 287. 942	695	354	817 899	763	463	1461	459	9457	9455	9492	9452	884 9119	809. 854	772	1722 1752	3639
															•	•	• •	• •	• •	٠.		•		-:0:	~ .0		4.0			N N
																,	•													
																		•												
7 														-														-		
PR PR PR PR PR	אם אם אם אם	תק תק	1d	וֹמְ וֹמְ	طِ	י סי ס <i>י</i>	יי טי ט	ם יים יים	ייר נסי נס												-									
ק ק ק ק ק ק ק ק ק ק ק	자 자 자 자 다 자 다	אס אס אס	PR	אָל אַר אַר	PR	אַק	איזי איזי איזי	קל קל	PR	PR PR	PR	יא PR PR	מק אק	PR PR	PR	PR PR	אק אק	PR PR	PR	PR	PR	אַס	אי ק אין	מי מינ	PR	מט איל	PR	ਸੂਬ	PH	
PR 25-0 PR 25-0 PR 26-0 PR 26-0 PR 26-0	PR 22-0 PR 22-0 PR 22-0 PR 22-0	PR 21- PR 21-	PR 21-	PR 14-	PR 14- PR 14-	PR 13-	PR 13.	PR 08	PR 05	PR 29	PR 24	72 Ad	PR 16	PR 10	PR 0	PR 3	PR 2	PR 2	PR 2	ря 2 2	יי סי טי א א א	PR 1	יי איי	אי איני	PR	PR PR	ר ק קים קים	PR	PR PR	ਹ ਸ਼ਹੀ ਸ
88888	2-00	2000	000	440	14-0	13-0	13-0	08-0	06-0	29-9	24-	22-	16-	10-	01-	ωω. 1-	27-	26	253	20	20	17 18	16	13	11	700	200	20	000	000
88888	2-00	2000	000	440	14-0	13-0	13-0	08-0	06-0	29-9	24-	22-	16-	10-	01-	ωω. 1-	27-	26	253	20	20	17 18	16	13	11	700	200	20	000	000
88888	2-00	2000	000	440	14-0	13-0	13-0	08-0	06-0	29-9	24-	22-	16-	10-	01-	ωω. 1-	27-	26	253	20	20	17 18	16	13	11	700	200	20	000	000
5-OCT-1999; 6-OCT-1999; 5-OCT-1999; 5-OCT-1999; 6-OCT-1999;	1-0CT-1999; 2-0CT-1999; 2-0CT-1999; 2-0CT-1999;	1-OCT-1999; 1-OCT-1999; 1-OCT-1999;	1-0CT-1999;	4-OCT-1999;	14-OCT-1999; 14-OCT-1999;	13-OCT-1999; 13-OCT-1999; 14-OCT-1999;	13-OCT-1999; 13-OCT-1999;	07-0CT-1999; 08-0CT-1999;	05-OCT-1999; 06-OCT-1999;	29-SEP-1999; 04-OCT-1999;	24-SEP-1999; 28-SEP-1999;	22-SEP-1999; 22-SEP-1999;	15-SEP-1999; 16-SEP-1999;	10-SEP-1999; 13-SEP-1999;	01-SEP-1999; 07-SEP-1999;	30-AUG-1999;	27-AUG-1999	26-AUG-1999 27-AUG-1999	23-AUG-1999 25-AUG-1999	20-AUG-1999 23-AUG-1999	20-AUG-1999 20-AUG-1999	17-AUG-1999 18-AUG-1999	16-AUG-1999	13-AUG-1999	11-AUG-1999	09-AUG-1999	06-AUG-199	05-AUG-199	04-AUG-199 05-AUG-199	03-AUG-199
5-OCT-1999; 990 5-OCT-1999; 990 5-OCT-1999; 990 6-OCT-1999; 990	1-OCT-1999; 990 2-OCT-1999; 990 2-OCT-1999; 990	1-OCT-1999; 990 1-OCT-1999; 990 1-OCT-1999; 990	1-0CT-1999; 991 1-0CT-1999; 991	14-OCT-1999; 99 14-OCT-1999; 99	14-OCT-1999; 99 14-OCT-1999; 99	13-0CT-1999; 99 13-0CT-1999; 99 14-0CT-1999; 99	12-0CT-1999; 99 13-0CT-1999; 99	07-0CT-1999; 99 08-0CT-1999; 99	05-OCT-1999; 99 06-OCT-1999; 99	29-SEP-1999; 90 04-OCT-1999; 90	24-SEP-1999; 9:	20-SEP-1999; 9 22-SEP-1999; 9 23-SEP-1990; 9	15-SEP-1999; 9 16-SEP-1999; 9	10-SEP-1999; 9	01-SEP-1999; 9	30-AUG-1999; 9	27-AUG-1999; 27-AUG-1999;	26-AUG-1999; 27-AUG-1999;	23-AUG-1999; 25-AUG-1999;	20-AUG-1999; 23-AUG-1999;	20-AUG-1999; 20-AUG-1999;	17-AUG-1999; 18-AUG-1999;	13-AUG-1999; 16-AUG-1999;	13-AUG-1999; 13-AUG-1999;	11-AUG-1999;	09-AUG-1999;	06-AUG-1999; 06-AUG-1999;	05-AUG-1999;	04-AUG-1999; 05-AUG-1999;	03-AUG-1999;
5-OCT-1999; 99US-01 5-OCT-1999; 99US-01 5-OCT-1999; 99US-01 5-OCT-1999; 99US-01	1-0CT-1999; 99US-01 2-0CT-1999; 99US-01 2-0CT-1999; 99US-01 2-0CT-1999; 99US-01	1-OCT-1999; 99US-0 1-OCT-1999; 99US-0 1-OCT-1999; 99US-0	1-OCT-1999; 99US-0 21-OCT-1999; 99US-0	14-OCT-1999; 99US-0 14-OCT-1999; 99US-0	14-OCT-1999; 99US-0 14-OCT-1999; 99US-0	13-OCT-1999; 99US-0 13-OCT-1999; 99US-0 14-OCT-1999; 90US-0	12-0CT-1999; 99US-0 13-0CT-1999; 99US-0	07-0CT-1999; 99US-0 08-0CT-1999; 99US-0	05-0CT-1999; 99US-(29-SEP-1999; 99US-(04-OCT-1999; 99US-(24-SEP-1999; 99US- 28-SEP-1999; 99US-	20-SEP-1999; 99US- 22-SEP-1999; 99US-	15-SEP-1999; 99US- 16-SEP-1999; 99US-	10-SEP-1999; 99US- 13-SEP-1999; 99US-	01-SEP-1999; 99US- 07-SEP-1999; 99US-	30-AUG-1999; 99US-	27-AUG-1999; 990S- 27-AUG-1999; 990S-	26-AUG-1999; 99US- 27-AUG-1999; 99US-	23-AUG-1999; 99US 25-AUG-1999; 99US	20-AUG-1999; 99US 23-AUG-1999; 99US	20-AUG-1999; 99US 20-AUG-1999; 99US	17-AUG-1999; 99US 18-AUG-1999; 99US	13-AUG-1999; 99US 16-AUG-1999; 99US	12-AUG-1999; 99US 13-AUG-1999; 99US	11-AUG-1999; 99US	09-AUG-1999; 99US	06-AUG-1999; 99Ug	05-AUG-1999; 99UG	04-AUG-1999; 99U 04-AUG-1999; 99U 05-AUG-1999; 90U	03-AUG-1999; 99U
5-OCT-1999; 99US-01 5-OCT-1999; 99US-01 5-OCT-1999; 99US-01 5-OCT-1999; 99US-01	1-0CT-1999; 99US-01 2-0CT-1999; 99US-01 2-0CT-1999; 99US-01 2-0CT-1999; 99US-01	1-OCT-1999; 99US-0 1-OCT-1999; 99US-0 1-OCT-1999; 99US-0	1-OCT-1999; 99US-0 21-OCT-1999; 99US-0	14-OCT-1999; 99US-0 14-OCT-1999; 99US-0	14-OCT-1999; 99US-0 14-OCT-1999; 99US-0	13-OCT-1999; 99US-0 13-OCT-1999; 99US-0 14-OCT-1999; 90US-0	12-0CT-1999; 99US-0 13-0CT-1999; 99US-0	07-0CT-1999; 99US-0 08-0CT-1999; 99US-0	05-0CT-1999; 99US-(29-SEP-1999; 99US-(04-OCT-1999; 99US-(24-SEP-1999; 99US- 28-SEP-1999; 99US-	20-SEP-1999; 99US- 22-SEP-1999; 99US-	15-SEP-1999; 99US- 16-SEP-1999; 99US-	10-SEP-1999; 99US- 13-SEP-1999; 99US-	01-SEP-1999; 99US- 07-SEP-1999; 99US-	30-AUG-1999; 99US-	27-AUG-1999; 990S- 27-AUG-1999; 990S-	26-AUG-1999; 99US- 27-AUG-1999; 99US-	23-AUG-1999; 99US 25-AUG-1999; 99US	20-AUG-1999; 99US 23-AUG-1999; 99US	20-AUG-1999; 99US 20-AUG-1999; 99US	17-AUG-1999; 99US 18-AUG-1999; 99US	13-AUG-1999; 99US 16-AUG-1999; 99US	12-AUG-1999; 99US 13-AUG-1999; 99US	11-AUG-1999; 99US	09-AUG-1999; 99US	06-AUG-1999; 99Ug	05-AUG-1999; 99U	04-AUG-1999; 99U 04-AUG-1999; 99U 05-AUG-1999; 90U	03-AUG-1999; 99U
5-OCT-1999; 99US-01 5-OCT-1999; 99US-01 5-OCT-1999; 99US-01 5-OCT-1999; 99US-01	1-0CT-1999; 99US-01 2-0CT-1999; 99US-01 2-0CT-1999; 99US-01 2-0CT-1999; 99US-01	1-OCT-1999; 99US-0 1-OCT-1999; 99US-0 1-OCT-1999; 99US-0	1-OCT-1999; 99US-0 21-OCT-1999; 99US-0	14-OCT-1999; 99US-0 14-OCT-1999; 99US-0	14-OCT-1999; 99US-0 14-OCT-1999; 99US-0	13-OCT-1999; 99US-0 13-OCT-1999; 99US-0 14-OCT-1999; 90US-0	12-0CT-1999; 99US-0 13-0CT-1999; 99US-0	07-0CT-1999; 99US-0 08-0CT-1999; 99US-0	05-0CT-1999; 99US-(29-SEP-1999; 99US-(04-OCT-1999; 99US-(24-SEP-1999; 99US- 28-SEP-1999; 99US-	20-SEP-1999; 99US- 22-SEP-1999; 99US-	15-SEP-1999; 99US- 16-SEP-1999; 99US-	10-SEP-1999; 99US- 13-SEP-1999; 99US-	01-SEP-1999; 99US- 07-SEP-1999; 99US-	30-AUG-1999; 99US-	27-AUG-1999; 990S- 27-AUG-1999; 990S-	26-AUG-1999; 99US- 27-AUG-1999; 99US-	23-AUG-1999; 99US 25-AUG-1999; 99US	20-AUG-1999; 99US 23-AUG-1999; 99US	20-AUG-1999; 99US 20-AUG-1999; 99US	17-AUG-1999; 99US 18-AUG-1999; 99US	13-AUG-1999; 99US 16-AUG-1999; 99US	12-AUG-1999; 99US 13-AUG-1999; 99US	11-AUG-1999; 99US	09-AUG-1999; 99US	06-AUG-1999; 99Ug	05-AUG-1999; 99U	04-AUG-1999; 99U 04-AUG-1999; 99U 05-AUG-1999; 90U	03-AUG-1999; 99U
PR 25-OCT-1999; 99US-0161405. PR 25-OCT-1999; 99US-0161405. PR 25-OCT-1999; 99US-0161406. PR 26-OCT-1999; 99US-0161360. PR 26-OCT-1999; 99US-0161360.	1-0CT-1999; 99US-01 2-0CT-1999; 99US-01 2-0CT-1999; 99US-01 2-0CT-1999; 99US-01	1-OCT-1999; 99US-0 1-OCT-1999; 99US-0 1-OCT-1999; 99US-0	1-OCT-1999; 99US-0 21-OCT-1999; 99US-0	14-OCT-1999; 99US-0 14-OCT-1999; 99US-0	14-OCT-1999; 99US-0 14-OCT-1999; 99US-0	13-OCT-1999; 99US-0 13-OCT-1999; 99US-0 14-OCT-1999; 90US-0	12-0CT-1999; 99US-0 13-0CT-1999; 99US-0	07-0CT-1999; 99US-0 08-0CT-1999; 99US-0	05-0CT-1999; 99US-(29-SEP-1999; 99US-(04-OCT-1999; 99US-(24-SEP-1999; 99US- 28-SEP-1999; 99US-	20-SEP-1999; 99US- 22-SEP-1999; 99US-	15-SEP-1999; 99US- 16-SEP-1999; 99US-	10-SEP-1999; 99US- 13-SEP-1999; 99US-	01-SEP-1999; 99US- 07-SEP-1999; 99US-	30-AUG-1999; 99US-	27-AUG-1999; 990S- 27-AUG-1999; 990S-	26-AUG-1999; 99US- 27-AUG-1999; 99US-	23-AUG-1999; 99US 25-AUG-1999; 99US	20-AUG-1999; 99US 23-AUG-1999; 99US	20-AUG-1999; 99US 20-AUG-1999; 99US	17-AUG-1999; 99US 18-AUG-1999; 99US	13-AUG-1999; 99US 16-AUG-1999; 99US	12-AUG-1999; 99US 13-AUG-1999; 99US	11-AUG-1999; 99US	09-AUG-1999; 99US	06-AUG-1999; 99Ug	05-AUG-1999; 99U	04-AUG-1999; 99U 04-AUG-1999; 99U 05-AUG-1999; 90U	03-AUG-1999; 99U
5-OCT-1999; 990 5-OCT-1999; 990 5-OCT-1999; 990 6-OCT-1999; 990 6-OCT-1999; 990	1-0CT-1999; 99US-01 2-0CT-1999; 99US-01 2-0CT-1999; 99US-01 2-0CT-1999; 99US-01	1-OCT-1999; 99US-0 1-OCT-1999; 99US-0 1-OCT-1999; 99US-0	1-OCT-1999; 99US-0 21-OCT-1999; 99US-0	14-OCT-1999; 99US-0 14-OCT-1999; 99US-0	14-OCT-1999; 99US-0 14-OCT-1999; 99US-0	13-OCT-1999; 99US-0 13-OCT-1999; 99US-0 14-OCT-1999; 90US-0	12-0CT-1999; 99US-0 13-0CT-1999; 99US-0	07-0CT-1999; 99US-0 08-0CT-1999; 99US-0	05-0CT-1999; 99US-(29-SEP-1999; 99US-(04-OCT-1999; 99US-(24-SEP-1999; 99US- 28-SEP-1999; 99US-	20-SEP-1999; 99US- 22-SEP-1999; 99US-	15-SEP-1999; 99US- 16-SEP-1999; 99US-	10-SEP-1999; 99US- 13-SEP-1999; 99US-	01-SEP-1999; 99US- 07-SEP-1999; 99US-	30-AUG-1999; 99US-	27-AUG-1999; 990S- 27-AUG-1999; 990S-	26-AUG-1999; 99US- 27-AUG-1999; 99US-	23-AUG-1999; 99US 25-AUG-1999; 99US	20-AUG-1999; 99US 23-AUG-1999; 99US	20-AUG-1999; 99US 20-AUG-1999; 99US	17-AUG-1999; 99US 18-AUG-1999; 99US	13-AUG-1999; 99US 16-AUG-1999; 99US	12-AUG-1999; 99US 13-AUG-1999; 99US	11-AUG-1999; 99US	09-AUG-1999; 99US	06-AUG-1999; 99Ug	05-AUG-1999; 99U	04-AUG-1999; 99U 04-AUG-1999; 99U 05-AUG-1999; 90U	03-AUG-1999; 99U

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR
PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-775-693-1 x AAG08821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAG08821 from: 1 to: 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAB53535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 lyGlnGlyIleLysGluLeuGluGlyLeuGluGlnLysAlaLysAlaSer 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 GCCAGAAG...GAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 pLeuLysGluAsnTyrGlyCysGluValValCysPheThrAlaAspValG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 GlyAlaSerGlnLeuValValAsnAspLeuThrGluGluPheValLysAs 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 ValAlaAlaGluValGlyAlaAspAlaValAlaHisGlyCysThrGlyLy 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 euLeuGlyThrSerMetAlaArgProValIleAlaLysAlaMetValAsp 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 ValValLeuAlaTyrSerGlyGlyLeuAspThrSerVallleValProTr 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                              513 CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                                                    245 GlnGlyArgGluAspAlaIleGluTyrAlaLysLysHisAsnValProVa 261
                                                                                                                                                                                                                                                                                                                                                                              463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCAT 512
                                                    295 AspMetTyr 297
                                                                                                    613 GGTCTCTAC 621
                                                                                                                                               278 euSerHisGluGlyAspLeuLeuGluAspProAlaAsnGluProLysLys 294
                                                                                                                                                                                            563 TCAGCTACGAGGCTGGAATCCTGGAGAACCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCGCCCAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pPheIlePheProCysLeuArgAlaGlyAlaIleTyrGluArgLysTyrL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sGlyAsnAspGlnValArgPheGluLeuThrPhePheSerLeuAsnProG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                         lProValThrLysLysSerIleTyrSerArgAspIleAsnLeuTrpHisL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0161992.
99US-0161993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0162142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533.00
3.270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 50.246
```

```
seq_documentation_block:
AAB53535 standard; Protein; 146 AA.
```

```
PD
XX
PF
                                                                                                                                                                                                                                                                                                                                                                                                                     identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer antigen protein sequence SEQ ID NO:1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder;
                                                                                                                                                                                                                                                                                                                                                          WO200055351-A1
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                           infectious disease; cardiovascular disorder
                                                                                                                                                                                                                                                                                                                   08-MAR-2000; 2000WO-US05883.
                                                                                                                                                                                                                                                                                                                                      21-SEP-2000.
                                                                                                                                                                                                                                           WPI; 2000-587534/55.
                                                                                                                                                                                                                                                                                                  12-MAR-1999;
                                                                                                                                                                                                                                                             Rosen CA, Ruben SM:
                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                    99US-0124270.
```

Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon diagnosis of colon cancer. N-PSDB; AAC98292. disorders such as colon cancer -

Claim 11; Page 1660-1661; 2104pp; English.

can be used in gene therapy. The colon cancer antigen polynicleotides, proteins and antibodies to the proteins are useful for the prevention, proteins and antibodies to the proteins are useful for the prevention, proteins and antibodies of colon disorders, such as colon cancer. The treatment and diagnosis of colon disorders, such as for polynicleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular diseases such as neural disorders, system disorders, muscular disorders, reproductive disorders gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, neuroprotective, immunomodulatory, gynaecological, gastrointestinal, wulnerary, nephrotropic, antiinfective and antibacterial activities, and vulnerary, nephrotropic, antiinfective and antibacterial activities, and

Sequence 146 AA;

```
alignment_scores:
                                                                                                alignment_block:
US-09-775-693-1 x AAB53535
                                                                           Align seg 1/1 to: AAB53535 from: 1 to: 146
                                                                                                                            Percent Similarity:
838 GGTATCTACGAGACCCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGA 887
                                      Quality:
                                                                                                                                      Ratio:
                                                                                                                              4.926
94.949
                                                                                                                                                  463.00
                                                                                                                       percent Identity: 92.929
                                                                                                                                                   Length:
                                                17
```

```
seq_documentation_block:
ID AAM16101 standard; Protein; 59 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name:
                                                               The present invention relates to human single exon nucleic acid probes (SEMP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SEMPs are derived from human HeLa cells. The SEMPs measuring human gene exingle exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical useful in grading and/or staging of diseases of the cervix, notably
 Sequence
                   at ftp.wipo.int/pub/published_pct_sequences.
                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                    Claim 27; SEQ ID No 20927; 487pp; English.
                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000US-0180312,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1088 GGGAGTCCCCACTGTCTCTCTACAATGAGGAGCTGGTGAGCATGAAC 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1038 AGGGAAAGTGCAGGTGTCCGTCCTCAAGGGCCCAGGTGTACATCCTCGGCC 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide #2535 encoded by probe for measuring cervical gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM16101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            988 GAGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGA 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 rgGluSerProLeuSerLeuTyrAsnGluGluLeuValSerMetAsp 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 GluCysGluPhevalArgHisCysIleAlaLysSerGlnGluArgValGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTTACGGCCTAGCCCT 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM16101
                                                                                                                                                                                                            gene expression in human cervical epithelial cells
59 AA;
                                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                            2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                     2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                                                                                                                                                                                                                                                     Chen W, Rank DR;
```

alignment_scores:

```
seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM28592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AAM16101 from: 1 to: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-775-693-1/rev x AAM16101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
       The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                              Claim 27; SEQ ID No 28861; 654pp; English.
                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                 analyzing
                                                                                                                                                                         WPI; 2001-488897/53.
                                                                                                                                                                                                      Penn SG,
                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                      04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                     03-AUG-2000; 2000US-0632366
21-SEP-2000; 2000US-0234687
27-SEP-2000; 2000US-0236359
                                                                                                                                                                                                                                                                                                   03-AUG-2000;
                                                                                                                                                                                                                                                                                                                            26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001.
                                                                                                                                                                                                                                                                                                               30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #2629 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM28592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM28592 standard; Protein; 59 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423 GACCTTTATCTGGGG 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473 TTGCGGCCCTTGAACCGGTTGTAGAATTCAGGCATCCTCCAGGGAGCAAT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  523 GAGTGACCGGGATGGGAATCCCGTGTTGCTTTGCGTACTCCATCAGGTCA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       573 CTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGGGTTCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AspLeuAsnLeuGly 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 leAlaAlaIleGluProValValGluLeuGlyHisProProGlySerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 uSerAspTrpAspGlyAsnProMetLeuLeuCysValPheHisGlnIleI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                          gene expression in human placenta -
                                                                                                                                                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                                              2000US-0608408
                                                                                                                                                                                                                                                                                                                                        2000US-0180312
                                                                                                                                                                                                                                                                                                                           2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228.00
4.560
                                                                                                                                                                                                  Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 76.364
                                                                                                                                                                                               Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50
```

•,"

SS

Sequence

59 AA;

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-775-693-1/rev x AAM28592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM03828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity: 90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAM28592 from: 1 to: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 573 CTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGGGTTCTTGG 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523 GAGTGACCGGGATGGGAATCCCGTGTTGCTTTGCGTACTCCATCAGGTCA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 TTGCGGCCCTTGAACCGGTTGTAGAATTCAGGCATCCTCCAGGGAGCAAT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423 GACCTTTATCTGGGG 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probe; human; breast disease; breast cancer; development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #2510 encoded by probe for measuring breast gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM03828 standard; Protein; 59 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LeuIleAlaAspThrHisGluValLeuValHisAspProArgValLeuGl 17
                                                                                                                                                                                                                                                                                                       29-JAN-2001; 2001WO-US00661.
  The present invention relates to novel single exon nucleic acid probes (see AAI100010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in
                                                      Claim 27; SEQ ID No 12568; 322pp; English.
                                                                                           Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                        WPI; 2001-476286/51.
                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspLeuAsnLeuGly 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                             2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                                2000US-0180312.
                                                                                                                                                                                                     2000GB-0024263.
                                                                                                                                                                                                                                                                   2000US-0207456
                                                                                                                                                                                                                   2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.560
                                                                                                                                                   Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 76.364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
```

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAB59826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAM03828 from: 1 to: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            percent Similarity:
PN XX PD XX PF PR XX XX PR PR XX XX PR DR XX XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-775-693-1/rev x AAM03828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              breast disease and non-carcinoma tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      573 CTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGGGTTCTTGG 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     523 GAGTGACCGGGATGGGAATCCCGTGTTGCCTTTGCGTACTCCATCAGGTCA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473 TTGCCGCCCTTGAACCGGTTGTAGAATTCAGGCATCCTCCAGGGAGCAAT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423 GACCTTTATCTGGGG 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 uSerAspTrpAspGlyAsnProMetLeuLeuCysValPheHisGlnIleI 34
                                                                                                                                                                                                                                                                                  Geobacter metallireducens.
                                                                                                                                                                                                                                                                                                                                                Toluene degradation; enzyme; waste degradation; TutE; TutD
                                                                                                                                                                                                                                                                                                                                                                                    Protein #3 encoded by TutD/E gene.
                                                                                                                                                                                                                                                                                                                                                                                                                     04-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB59826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB59826 standard; Protein; 1615 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 leAlaAlaIleGluProValValGluLeuGlyHisProProGlySerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LeuIleAlaAspThrHisGluValLeuValHisAspProArgValLeuGl 17
                                                                                                                                                                                                                                                                                                                      Thauera aromatica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                   24-MAY-2000; 2000WO-US14298.
                                                                                                                                                                                                                                                                     Azoarcus tolulyticus.
                                                                                                                                                                                                                                                                                                  Xanthomonas maltophilia
                                                                                                                                  01-JUN-1999;
                                                                                                                                                                                                     07-DEC-2000.
                                                                                                                                                                                                                                     WO200072650-A2.
                 N-PSDB; AAF23627
                                  WPI; 2001-041080/05.
                                                                Coschigano PW;
                                                                                                  (UYOH-) UNIV OHIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspLeuAsnLeuGly 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228.00
4.560
90.909
                                                                                                                                      99US-0323872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 76.364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
```

354 CACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCA 391
25 ValSerThrThrSerProArgSer1
'sProArgProT}
94 CGCCC
262 CTCCTGGGCACCTCTCTTGCCAGGCCCTGCAT 293 691 oSerTrpLysThrGlyCysTrpArgAlaSerSerSerProLysSerIleS 708
675 ArgArgProSerLeuProValThrThralaSerCysArgProThrLysPr 691
58
110 ACATTGGCCAGAAGAACTTCGAGGAAGCCAGGAAGAAGGCACTG 156 :::
111
_
5 CCAGCAAAGGCTCCGT(::: 8 ProSerValalaargT1
•
alignment_block: US-09-775-693-1 x AAB59826
allgnment_scores: Quality: 205.50 Ratio: 0.943 Percent Similarity: 41.843 Percent Identity: 23.800
Sequence 1615 AA;
degrading enzymes are useful ds and in particular for the contained in liquid or solid ortein sequence encoded by tol
The present invention relates to toluene degrading enzyme ge proteins tuth (see AAF23629 and AAB59831), tutl (AAF23630 an tuth (AAF23631 and AAB59833) and tutc (AAF23632 and AAB59834 toluene degrading enzymes are hearly (AAF23632 and AAB59834
Disc
PT Composition comprising toluene degrading enzyme useful for biological PT treatment of organic compounds, especially for degrading toluene or its XX

CCGTCCTCAAGGGCCAGG 107
9/9 CCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAGTC 1022
133 GUTGGGCTTGAAATTTGCTGAGCTGGTGTAT ::::: 18 AlaArgArgProVallleSerArgArgSe
08ACCGGAAGTGCGCA. 101 ysSerArgSerMetThrAlaThrThrGlyArgThrPro
159 GGCACCATCCTTTACCATGCTCAT
109 AGAACCGCTTCATTGGAATGAAC
759 CCTGAACO
"15 AAGGATGGCACCACCCACC : 40 rArgSerAlaArgSerArg
TTCTCGAGATC
CAACACCCCTGACA ::: ::::::::::::::::::::::::::::::
O/ CCTCCAGGTCTCTACACGAAGACCCAGG 1 ::: ::: 91 oThrProSerSerArgGlnProSerGlySer
SerProSerAlaAlaProThrProArgA
58 erArgalaProThra
81 ATGGAGTACGCAAAG ::::: 41 GTrpAsnSerSerArgTr
108 laThrArgAlaAlaThrProArgArgLysTh
GThrargCysargArgAsnSe
75 SerProThrSerValSerAlaPheProProSerProAlaAr

```
seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAB59813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                   alignment_scores:
                                                                         alignment_block:
US-09-775-693-1 x AAB59813
                                                                                                                    Quality:
Ratio:
Percent Similarity:
                                         Align seg 1/1 to: AAB59813 from: 1 to: 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1062 Cys......ArgCysLeuSerCysProGlnSerTh 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1073 TGTACATCCTCGGCCGGGAGTCCCCCACTGTCTC......TCTAC 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1050 roArgThr......CysArgAlaThrSerSerAlaSer 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1111 AATGAGGAGCTGG 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1071 rThrAlaAlaTrp 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB59813 standard; Protein; 1017 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toluene degradation; enzyme; waste degradation; TutD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB59813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TutD protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas maltophilia.
Geobacter metallireducens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-2000; 2000WO-US14298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200072650-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Azoarcus tolulyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thauera aromatica
                                                                                                                                                                                                                                                          The present invention relates to toluene degrading enzyme genes and proteins tuth (see AAF23629 and AAB59831), tutl (AAF23630 and AAB59832), tutl (AAF23631 and AAB59833) and tutl (AAF23632 and AAB59834). The toluene degrading enzymes are homologues of pyruvate formate lyase. The toluene degrading enzymes are useful for biological treatment of organic toluene degrading enzymes are useful for biological treatment of organic compounds and in particular for the degradation of toluene and its analogs contained in liquid or solid waste source. The present sequence analogs contained in liquid or solid waste source. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               Composition comprising toluene degrading enzyme useful for biological treatment of organic compounds, especially for degrading toluene or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coschigano PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYOH-) UNIV OHIO.
                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 5; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       analogs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAF23625, AAF23627.
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                              is a protein sequence for toluene degrading enzyme, TutD
           38 GCGGCCTGGACACCTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTAT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-041080/05
:::== ===:::
                                                                                                                                                                                                                     1017 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9905-0323872.
                                                                                                                         193.00
0.910
42.656
                                                                                                                           Percent Identity: 23.944
                                                                                                                                                            Length:
        .....
                                                                                                                                               497
29
```

578 267 537 250

316 664 299 628 284

```
seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:AAW87504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
Daggett LP,
                                    (SIBI-) SIBIA NEUROSCIENCES INC
                                                                                          20-APR-1994;
20-APR-1993;
                                                                                                                                                          20-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1095 CCCACTGTCTC......TCTACAATGAGGAGCTGG 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1045 GTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTC 1094
                                                                                                                                                                                                           15-DEC-1998.
                                                                                                                                                                                                                                                       US5849895-A.
                                                                                                                                                                                                                                                                                                                                                    Human; N-methyl-D-aspartate receptor; NMDAR2C;
                                                                                                                                                                                                                                                                                                                                                                                       Human N-methyl-D-aspartate receptor subunit encoded by clone NMDA24.
                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                       NMDA-activated cation-selective ion channel; glutamate receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 ..ArgCysLeuSerCysProGlnSerThrThrAlaAlaTrp 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW87504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW87504 standard; Protein; 1061 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455 .CysArgAlaThrSerSerSerAlaSerCys...... 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  443 AsnMetArgSerThrSerValSerAlaProArgThr.......... 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                995 AATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGGAAA 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426 erArgArgSerProSerArgMetPheGlyArgLeuSerAlaSerSerIle 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    957 GCTGGTGTATACCG.....GTTTACGGC.....CTAGCCCTGAGTGTG 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 rThrGlyArgThrProThrCysAsnSerAlaArgArg...ProValIleS 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908 ACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGA 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 AlaGlnSerSerArgProSerCysTrpLysSerArgSerMetThrAlaTh 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               881 ATTTAGACATCGAGGCCTTCACCATGG....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  831 GTCCCGAGGTATCTACGAGACCCCCAGCAGGCACCATCCTTTACCATGCTC 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 oThrThrGlySerThrCysCysAlaCysArgProAlaSer..... 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            781 CATGGCGTGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGAA 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 AsnThrProSerSerAlaSerThrAlaThrAlaProProThrArgLysPr 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       737 .....CCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAG 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333 spSerAlaIleArgArgSerSerThrThrArgSerAlaArgSerArgArg 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 gArgThrAlaArgArgArgCysAlaGlyPheSerSerAlaSerAlaThrA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     665 .....TTCTCGAGATCGAGTTCAAAAA 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....ThrValAlaAlaArg...ArgLysLysProValArgLysValAla 393
                                                                                94US-0231193.
93US-0052449.
                                                                                                                                                        94US-0231193.
```

```
(AAV8289) inserted between nucleotides 23050 and 2351, as set forth in subunits contribute to the formation of NWDA-activated cation-selective receptor subunit proteins, the nucleic acids are also useful as probes to Functional glutamate receptors can be assembled from several NMDA subunit proteins of one type (homomeric) or from combinations of also comprises methods for using such receptor subunit proteins of one type (homomeric). The present invention also comprises methods for using such receptor subunits of also comprises methods for determining whether receptors, e.g. invention also comprises methods for determining whether unknown
    Sequence
                         protein(s) are functional as NMDA receptor subunits.
                                                                                                                                                                                                                                                                                                   The present sequence represents a human N-methyl-D-aspartate (NMDA) receptor subunit (NMDAR). The nucleic acid sequence does not contain the 860 5'-most nucleotides, has an additional 11 nucleotides (AAV82891) between nucleotides 1300 and 1301, an additional 24 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Columns 261-268; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding N-methyl-D-aspartate receptor subunit - useful for the assembly of functional glutamate receptor subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV82910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-069812/06.
1061 AA;
```

alignment_block: US-09-775-693-1 x AAW87504 alignment_scores: Align seg 1/1 to: AAW87504 from: 1 to: 1061 Percent Similarity: 624 sProSerTrpThrSerCysTrpLeuSerAlaGlyAlaSerThrAlaAlaS 641 352 GCCACAGGAAAGGGGAACG...ATCAGGTCCGGTTTGAGCTCAGCTGCT. 397 610 SerThrTrpSer.....ThrGlySerCysAlaThrArgCysProThrHi 624 302 AACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCCACGGC 351 594 ..ThrCysCysTrpTrpProTrpGlyTrpProCysTrpSerSerProGly 609 252 GGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCA 301 582 aSerTrpThrSerThrThrTrpGluAlaSerSer...... 593 568 CysGlySerGlnGlySerAlaArg.....MetArgArgThrArgAlaAl 582 202 TTTGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGA 251 152 CACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAG 201 551 rpArgSerCysSerSerTrpGlyThrGluArgHisArgAsnTrpArgGln 105 GGCCAACATTGGCCAGAAGGAAGACTTCGAGG...AAGCCAGGAAGAAGG 151 536 rAlaSerProCys.....ArgArgThrProThrGlySerGlyProThrT 551 520 AlaSerTrpSerProLeuGlyLeuAlaArgSerLeuLeuProLeuAlaTh 536 55 TGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCT 104 38 GCGGCCTGGACACCT......CG 54 Quality: Ratio: 174.00 38.593 Percent Identity: 23.881 Length:

```
AAW87503 standard; PY
XX
AC AAW87503;
ACC
AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:AAW87503
                                                                                                                                                                                                          XX
The present sequence represents a human N-methyl-D-aspartate (NMDA)
CC receptor subunit (NMDAR). The nucleic acid sequence does not contain
CC the 366 5'-most nucleotides, by the insertion of 11 nucleotides between
CC the 366 5'-most nucleotides, by the insertion of 11 nucleotides between
CC 1960-1974, nor the 1061 3' nucleotides, as set forth in AAV82889. The
CC 1960-1974, nor the 1061 3' nucleotides, as set forth in AAV82889. The
CC cDNA sequence is derived from clone NMDA21. The NMDAR subunits contribute
CC cDNA sequence is derived from clone NMDA21. The NMDAR receptor subunit
CC cDNA sequence is derived from clone NMDA21. The SMDAR receptor subunit
CC contribute to being useful for the production of NMDA receptor subunit
CC addition to being useful for the production of NMDA receptor subunit
CC addition, the nucleic acids are also useful as probes to identify and
CC approteins, the nucleic acids are also several NMDA receptor subunit
CC isolate nucleic acids encoding related receptor subunits. Functional
CC glutamate receptors can be assembled from several NMDA receptor subunit
CC of different types (homomeric) or from combinations of subunit proteins
CC of different types (heteromeric). The present invention also comprises
CC compounds which affect the function of such receptors .e.g. agonists
CC antagonists and modulators of glutamate receptor function. The invention
CC antagonists methods for determining whether unknown protein(s) are
CC also comprises methods for determining whether unknown protein(s) are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1127 GCATGAACGTGCAGGGTGATTATGAGCCAACTGATGCCACCGGGTTCATC 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1177 AACATCA 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 905 .....ProAlaArgArgAlaSerArgGlnGlyProProProGlySerTh 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      919 rAspSer 921
              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW87503 standard; Protein; 1212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human N-methyl-D-aspartate receptor subunit encoded by clone NMDA22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NMDA-activated cation-selective ion channel; glutamate receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; N-methyl-D-aspartate receptor; NMDAR2C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-069812/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Daggett LP, Lu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SIBI-) SIBIA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Columns 253-262; 203pp; English.
                                                                                                                   Sequence 1212 AA;
                                                                                                                                                                                    functional as NMDA receptor subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-0231193.
93US-0052449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0231193.
Length:
Gaps:
```

Quality: 174.00 Ratio: 0.961

7,3

ر ٔ

Key Misc-diff Misc-diff	n_block: candard; [first first candard; [c	734 laGlyGlyThrSetArgProPro. SerGlyProCysGlyProGlyThr 934 laGlyGlyThrSetArgProPro. SerGlyProCysArgProArgAl 758
	subunit NMDARIA #18. NMDA: NMDARIA; ionotropic; animal model; disease diagnosis;	GlyargCysGlyProGlyThra 934 PCCTTGGAGCTCTTCATGT

```
Misc-difference
                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                              US6111091-A
                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                           Misc-difference
        Novel DNA fragment encoding human N-methyl-D-aspartate receptor subunit for identifying mutations and for developing drugs against various disease states
                                     N-PSDB;
                                                           Daggett LP,
                                                                                          20-APR-1994;
20-APR-1993;
                                                                                                                               29-AUG-2000
        disease states
                                                                          (MERI ) MERCK & CO INC
                                                                                                                29-SEP-1997;
                                             2000-578607/54
                                     AAA95033
                                                           Lu C;
                                                                                                                                                                                                                                                                                            /label= unknown
/note= "encoded;
> 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
274
                                                                                          94US-0231193.
93US-0052449.
                                                                                                                                                                                                                                                                                                                                          /note= "0
593..594
                                                                                                                97US-0940086
                                                                                                                                                                                                                                                                      /note= "encoded
858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "encoded 162
                                                                                                                                                                                                                                                                                                                                                                                                               /note=
337..3
                                                                                                                                                                                                                                                                                                                                                                  561
                                                                                                                                                                                                                                                                                                                                                                                         431
                                                                                                                                                                                                                                                                                                                                                                                                                                      313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183
                                                                                                                                                                                                   /note= "encoded 1076
                                                                                                                                                                                                                                                1001
                                                                                                                                                                                                                                                                                                                     692
                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                          1058
                                                                                                                                                                    /note= "the coding sequence of this protein contains
number of in-frame stop codons which are represented
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "encoded
                                                                                                                                                                                                                                                       /label= unknown
/note= "encoded
                                                                                                                                                                                                                                                                                                                                                                         /note= "encoded
                                                                                                                                                                                                                                                                                                                                                                                               /note= "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "encoded"
                                                                                                                                                                                    'note=
                                                                                                                                                                                             /label= UNKNOWN
                                                                                                                                                                                                                  /label= unknown
                                                                                                                                                                                                                                 'note= "encoded
                                                                                                                                                                                                                                         'label= unknown
                                                                                                                                                                                                                                                                                      ′label= unknown
                                                                                                                                                                                                                                                                                                                           'note= "encoded
                                                                                                                                                                                                                                                                                                                                    'label=
                                                                                                                                                                                                                                                                                                                                                          'label= unknown
                                                                                                                                                                                                                                                                                                                                                                                 'label≖ unknown
                                                                                                                                                                                                                                                                                                                                                                                                        'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label≖ unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                              label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                . 338
                                                                                                                                                                                                                                                                                                                                                  "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                      "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                             "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "encoded
                                                                                                                                                            in the protein sequence"
                                                                                                                                                                                    "encoded by TGA"
                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          γd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bу
                                                                                                                                                                                                                                                                                                                                                  bу
                                                                                                                                                                                                                                                                                                                                                                        bу
                                                                                                                                                                                                                                                                                                                                                                                                                      bу
                                                                                                                                                                                                                                                                                                                                                                                                                                             ьу
                                                                                                                                                                                                          þу
                                                                                                                                                                                                                                 by
                                                                                                                                                                                                                                                                                                     þу
                                                                                                                                                                                                                                                                                                                           þу
                                                                                                                                                                                                                                                                                                                                                                                               bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   уd
                                                                                                                                                                                                                                                       by TGA'
                                                                                                                                                                                                                                                                              by TAA"
                                                                                                                                                                                                                                                                                                                                                   TAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGA"
                                                                                                                                                                                                                                                                                                     TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                       TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                              TAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGA"
                                                                                                                                                                                                          TGA"
                                                                                                                                                                                                                                                                                                                                                                                               TGATGA"
                                                                                                                                                                                                                                  TAG"
                                                                                                                                                                                                                                                                                                                            TGATGA"
                                                                                                                                                                                                                                                                                                                                                                          TGA"
                                                                                                                                                                             ω
```

```
8 X 0 0 0 0 0 0 0 X 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-775-693-1 x AAB26240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a subunit (designated NMDARIA) of the human N-methyl-D-aspartate (NMDA) receptor. This is an ionotropic glutamate receptor which contains cation-specific ligand-gated ion channels. The protein and its coding sequence can be used in disease diagnosis and in research to identify other, similar proteins. They can also be used as probes, for example in genetic screening, and in drug screening, as well as enabling the production of animal disease models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 CCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         613 ProTrpGlyTrpPro.....CysTrpSerSerProGlySerThr..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              672 erArgProAlaArgProArgProAla.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; column 633-672; 205pp; English.
593 CCAAGA
                                        729 laProAlaHisAlaCysProProProThrArgProGlnSer...ArgAla
                                                                                                                                                                                                                                        467 GCCGCAATGACCTGATGGAGT.....ACGCAAAGCAACACGGGATT
                                                                                                                                                                                                                                                                                                                                                                                                          367 AACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..GlySerCysAlaThrArgCysProThrHis.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTG
                                                                                                                                                                                                                                                                                                                            AAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGG
                                                                                                                                                                                                                                                                                                                                                                  aThr....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCCACAGGAAAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt rAlaGlyCysArgAlaSerProAlaHisArgGlyArgProAlaArgThrS}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProSerTrpThrSerCysTrpLeuSerAlaGlyAlaSerThrAlaAlaSe
                                                                           GGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACC
                                                                                                                      lAlaAlaAlaValArgProHisArgProProAlaArgProArgGlyLeuA
                                                                                                                                                          C.....CCATCCCGGTCACTCCCAAGAACCCGTGGAGCAT
                                                                                                                                                                                                  Ala***AlaThrProTrpThrAlaProLeuAlaProSerArgIleGlyVa
                                                                                                                                                                                                                                                                                                                                                                                                                                            .....CysSerArgPheCysArgGlnProAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: AAB26240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1081 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....TrpSerThr....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157.50
0.984
35.794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 24
Percent Identity: 22.819
                                                                                                                                                                                                                                                                              .....Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to:
ACCAAGCGCCTCCAGGTCTC
                                                                                                                                                                                                                                                                                                                                                                  .....Trp***ProArg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                466
                                                                                                                                                                                                                                                                                                                                                                                                          416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116
    618
                                          744
                                                                                                                        729
                                                                                                                                                                542
                                                                                                                                                                                                                                                507
                                                                                                                                                                                                                                                                                      695
                                                                                                                                                                                                                                                                                                                                                                      694
                                                                                                                                                                                                                                                                                                                                                                                                                                                    689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as
well
```

745	ProArgAlaGlyAspArgGlnThrGlyValAlaArgArgLeuCysAlaGl 7	ത്
619	ACCCAGCCAAAGCC::::	າ ທ່
6 1	0.000000000000000000000000000000000000	, .
	**************************************	5 6
701		٠ ر
10/	AAGGATGGCACCACCCACCAG 7	ū
792	rgCysGlyProGlyThrAlaGlyGlyThrSerAr 8	õ
736	CCTCCTTGGAGCTCTTCATGT7	Ű.
804	roProSerGlyProCysArgProArgAlaValThrThrAlaProP 8	$\tilde{\mathbf{z}}$
758	TGAACGAAGTCGCGGGC	7
820	heLeuGluProThrAspProAlaAlaProSerSerArgSerSerArgSer 83	w
779	GTATTGACATCGTGGAGAAC 8	$\stackrel{\sim}{\vdash}$
837	TrpArgThrCysArgCysSerValArgSerSerTrpProGl 8	Ü
814	GACCCCAGCAGGCAC 8	6
853		6
864	ACCATGGACCGGG 9	$\dot{=}$
863	oTrpProArg 8	7
914	AAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGTG 9	6
879	8	7
964	CCTGAGTGTGAATTTGTCCGCCACT	0
088	roAlaArgCysProLeuGlyAlaProAlaP 8	9
014	AGTCCCAGGAGCGAGTGGAA	0
894	ProAlaProThrAlaThrArgProAlaGlyAlaTrpArgArg 9	دسو
043	GTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAG 1	0
911	ArgSerArgCysAla9	1
093	SAGCTGGTGAGCATGAACGTGCAGGG 1	سن
916	rgSerThrGlyArgProAlaArgA 9	2
143	TGATTATGAGCCAACTGATGCCACCGGGTTCATCAACATCA 1183	
925	rgAlaSerArgGlnGlvProProProGlvSerThrAspSer 938	

107.00

151.72 0.0531 151.72 0.0531

```
OM of: US-09-775-693-1 to: Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database: Issued_Patents_AA:*
Database sequences: 212252
Database length: 22503292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query length: 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search information block: Query: US-09-775-693-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Command line parameters:
                    /cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-931-820-1 + 116.50 167.93 0.0 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-963-825-18 + 116.50 167.05 0.0070 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-963-825-18 + 116.00 164.22 0.0080 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-931-820-1 + 113.00 161.78 0.0139 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-931-820-1 + 113.00 161.78 0.0139 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-09-01-820-4 + 113.00 161.78 0.0139 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-09-001-51-24 + 111.50 163.48 0.0159 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-09-001-51-24 + 111.50 163.48 0.0159 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-931-820-2 + 110.50 154.71 0.0241 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-931-820-2 + 110.50 157.71 0.0241 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-931-820-2 + 110.50 157.71 0.0241 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-866-881A-6 + 110.00 162.99 0.0203 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-866-881A-6 + 110.00 162.99 0.0203 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-208-887A-49 + 110.50 154.04 0.0412 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-208-887A-49 + 108.50 161.83 0.0266 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-313-288B-15 + 108.00 154.04 0.0412 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-313-288B-15 + 107.50 161.91 0.0366 (cgn2_6/ptcodata/2/i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Strd Orig ZScore EScore Len i Docume (Ggn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-219-849-7 + 140.00 / Cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-219-849-6 + 139.50 / Cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-041-886-23 + 139.00 / Cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-09-041-886-23 + 137.50 / Cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-09-413-814-78 + 134.00 / Cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-413-814-78 + 134.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search time (sec): 67.130000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-219-849-49 + /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-906-865-4 + /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-219-849-8 + /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-219-849-8 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pot
-THR_MAX=100 -THR_MIN=0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs
-NORM-ext -MINLEN-0 -MAXLEN-200000000
-USER-US0977593_@CGN1_1_22 -NCPU-6 -ICPU=3 -LONGLOG -NO_XLPXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09775693/runat_12022002_124152_1324/app_query.fasta_1.1315
-DB=-Tssued_patents_AA -QFMT=fastan -SUFFIX=ra1 -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH-0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/iaa/6A_COMB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WAIT -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       _6/ptodata/2/iaa/5A_COMB
_6/ptodata/2/iaa/6A__COMB.pep:US-08-851-843A-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002 3:52 PM
                                                                                                                                                                                                                                                                                                                                                                                                                               .pep:US-08-642-255-80 + 116.50
.pep:US-08-642-246-16 + 116.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 out_format : pts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 + 118.00
50 + 118.00
49 + 118.00
4 + 117.00
8 + 116.50
                                                                                                                                                                                                                                                                                                                                                                             118.00 173.77 0.0032
117.00 174.02 0.0044
116.50 168.60 0.0061
116.50 167.93 0.0062
116.50 167.93 0.0062
116.50 167.93 0.0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Documentation
140.00 217.88
139.50 210.22
        107.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.00 206.75
7.50 214.68
1.00 201.45
1.50 208.12
1.31 50 208.0
1.00 192.01
1.00 192.01
1.00 180.99
7.00 194.99
7.00 194.99
              50 161.83 0.0266

7 154.04 0.0412

50 161.91 0.0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.99 0.0006
94.99 0.0004
94.99 0.0004
94.99 0.0004
94.99 0.000
92.13 0.0005
84.05 0.0012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01.45 0.0001
08.12 0.0001
208.12 0.00
92.01 0.0003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.0e-05
3.1e-05
3.9e-05
3.3e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.0032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.0004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.0001
                                                                                                                                                                                                                                                                                                                                                                                                          .0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1065
1958
539
539
539
                                                                                      1064
1341
1057
1057
1057
739
739
1024
1366
618
621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  633
684
684
1078
1078
595
822
                                                                                                                                                                                                                                                                                                                                                                                                                            1008
1065
1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355
                                                                                                                                                                                                                                                                                                                                                                                                          106
```

```
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-974-549A-336+ 107.
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-854-050-217+ 107.0
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-029-348-3+ 106.00
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-029-348-2+ 106.00
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-525-742-6+ 105.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-219-849-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-775-693-1 x US-09-219-849-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-219-849-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-09-219-849-7 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Illustrative OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 SerArgAspProGlyProProGlyAlaHisGlyProAlaGlyProLysGl 130
                                                                                                                                                                                                                                                                                                                                                                           130 y......AlaHisGlyProAlaGlyProLysGlyAlaHisG
419 AGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGC
                                     178 ro.AlaGlyProGlyGlySerArg.....AspProGlyProProGly..
                                                                                                                     161 oAlaGlyProGlyGlySerArgAspProGlyProProGlyAlaGlnGlyP 178
                                                                                                                                                               319 CAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGAA
                                                                                                                                                                                                         269 GCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCC
                                                                                                                                                                                                                                                                                           142 lyProAlaGlyProLysGlyAlaHis.....
                                                                                                                                                                                                                                                                                                                              225 GGCCATCCAGTCCA......GCGCACTGTATGAGGACCGCTACCTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                       175 GTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGAGTTCATCTGGCC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 TCGAGGAAGCCAGGA.....AGAAGGCACTGAAGCTTGGGGGCCAAAAAG 174
                                                                             CGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCAGATAA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6150081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAN HEERDE, GEORGE V.
VAN RIJW, ALEXIS C.
BOUWSTRA, JAN B.
DE WOLF, FREDERIK A.
MOOBROEK, ANDREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09219849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WIND, RICHELE D.
VAN DEN BOSCH, TANJA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WERTEN, MARC W.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2728-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE REPARATION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334
22
26.946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155.76
155.70
163.25
                                                                                                                                                                        368
                                                                                                                                                                                                                161
                                                                                                                                                                                                                                                                                                  150
                                                                                                                                                                                                                                                                                                                                            268
                                                                                                                                                                                                                                                                                                                                                                                   142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .72 0.053
6 0.0509
0 0.0510
5 0.0386
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-219-849-6
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6150081
                    APPLICANT: MOOBROEK, ANDREAS
APPLICANT: WERTEN, MARC W.T.
APPLICANT: WIND, RICHELE D.
APPLICANT: VAN DEN BOSCH, TANJA J.
TITLE OF INVENTION: SUITVER HALLDE ENULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SUITNALE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
TITLE OF INVENTION: PREPARATION THEREOF
                                                                                                                                                                                                                                                  APPLICANT: VAN HEERDE, GEORGE V.
APPLICANT: VAN RIJN, ALEXIS C.
APPLICANT: BOUWSTRA, JAN B.
APPLICANT: DE WOLF, FREDERIK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1048 CAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCC 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         998 TTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTG 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 la...HisGlyProAlaGlyProLysGlyAla.....HisGlyProAla 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 GlyProLysGly.....AlaHisGlyProAlaGlyProLysGlyAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   748 CTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTAT 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 ProAlaGlyProGlyGlySerArgAsp.....ProGlyPro..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       604 GCGCCTCCAGGTCTCTACACGAAGACCCAGGACCC.....AGCCAAAGC 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 698 TGAAGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAG 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                648 CCCCAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCCTG 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 lyGlySerArg......AspProGlyProProGlyAlaGlnGly 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 GlyAlaGlnGlyProAlaGlyProGly.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          519 CACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCAGCT 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....ProAlaGlyProGlyGlySerArgAspProGlyProPro 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....ProGlyGlySerArgAspProGlyProProGlyAlaGlnGly. 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...GlyProAlaGly..... 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAAT 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ........GlyProGlyGlySerArgAspProGlyProProGlyAlaGln 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nGlyProAla.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGACCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ......ProGlyAlaHisGlyProAlaGlyProLysGlyA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roAlaGlyProGlyGly......SerArgAspProGlyProPro 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .GlySerArgAspProGlyProProGlyAlaGlnGlyProAlaGlyProG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCCATCCCGGT 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09219849
2728-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....AlaGlnGlyP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Illustrative; OTHER INFORMATION: amino acid sequence US-09-219-849-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-09-219-849-6 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-775-693-1 x US-09-219-849-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity: 36.695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 960
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                         347 lyProAlaGlyProGlyGlySerArg......AspProGlyPro
                                                   360 ProGlyAlaGlnGlyProAlaGlyProGlyGlySerArgAsp..... 373
                                                                                                                                                                                                                                                                       330 yProAlaGlyProGlyGlySerArgAspProGlyProProGlyAlaGlnG
                                                                                                                                                                                                                                                                                                                     297 roAlaGlyProGlyGlySerArgAspProGlyProProGlyAlaGlnGly 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 lyProAlaGlyProLysGlyAlaHis.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 GGCCATCCAGTCCA.....GCGCACTGTATGAGGACCGCTACCTCCTGG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 GTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGAGTTCATCTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 TCGAGGAAGCCAGGA.....AGAAGGCACTGAAGCTTGGGGCCAAAAAG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 SerArgAspProGlyProProGlyAlaHisGlyProAlaGlyProLysGl 232
                                                                                                                                                                                                                 ..CCCCAAGAACCAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCC 638
                                                                                                                                                                                                                                                                                                                                                                                                               GATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACC 553
AAAAAGGGGTCCC.....TGTGAAGGTGACCAACGTCAAGGATGGCACC 726
                                                                                                                                                                                                                                                                                                                                                                                ProAlaGlyProGlyGlySerArgAspProGlyProProGlyAlaGlnGl 330
                                                                                                           ....AGCCAAAGCCCCCAACACCCCTGACATTCTCGAGATCGAGTTCA 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ro.AlaGlyProGlyGlySerArg.....AspProGlyProProGly.. 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oAlaGlyProGlyGlySerArgAspProGlyProProGlyAlaGlnGlyP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....AlaGlnGlyP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGC 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGAA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y.....AlaHisGlyProAlaGlyProLysGlyAlaHisG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139.50
1.065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 357
Gaps: 20
Percent Identity: 26.050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      960
                                                                                                                                                              359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            503
```

57 TGCACAT	57 TGC
507 TCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCA 55	07
491CAAAGCAACACGGGAT 50 ::::: ::: 488 nGlnGlnGlnGlnGlnGlnGlnHisHisGlyAsnSerGlyProP 50	8 n
470 GCAATGACCTGATGGAGTACG	70 72
0 GGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCC	9
70 GATCAGGTCCGGTTTGAGCTCAGCTGGTACTCACTGGCCCCCCAGATAAA 4 :::	0 GATC ::: 0 gLeu
341	SerG
CGCCCGCAAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATG	e – G
44 CTGTATGAGGACCGCTACCTCCTGGGCACCTCTTTGCCAGGCCCTGCAT 2 :::::::::::::::::::::::::::::::::::	OA CT
94 GCAGGGAGTTTGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCA 24	4 4
59 GCTTGGGGCCAAAAAGG	9 G
AACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAA 15	0
TGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCC 10	71 TGAAGG 334 aMetGl
GGTTCTGGCCTACAGTGGCGGCGCCTGGACACCTCGTGCATCCTCGTGTGGC 70	
	eg
nt_b 775-	t_b 75-
ent_scores: Quality: 139.00 Ratio: 0.755 Ratio: 0.755 1t Similarity: 41.913 Percent Identity: 26.651	t_s si
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 1185 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein 9-04-041-886-23	; INFORMATION I SEQUENCE CI LENGTH: TYPE: A TOPOLOGY MOLECULE T US-09-041-886-2

COUNTRY: USA

```
seq_documentation_block:
    Sequence 12, Application US/08660963
    Patent No. 5852187
                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-660-963-12
                                                                                                                     GENERAL INFORMATION:
APPLICANT: Thorner, Michael O.
APPLICANT: Gaylinn, Bruce D.
APPLICANT: Horikawa, Reiko
APPLICANT: Lyons Jr., Charles E.
TITLE OF INVENTION: MOLECULAR CLONING OF THE OVINE PITUITARY
TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE RECPTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1135 GTGCAGGG 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1085 GCCGGGAGTCCCCACTGTCTCTCTACAATGAGGAGCTGGTGAGCATGAAC 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1035 GEAAGGGAAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCG 1084
STREET: G. Street CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         694 roAlaGly 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               681 sProGlySerProThrVal......GlyProGlyProLeuProp 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  670 GlyThrSerPro......ProAlaGlyProGlyThrPhe...Ly 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       656 .....SerProProSerPheArgThrGlyThrProProGlyTyrArg 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               991 TGTGAATTTGTCCGCCACTGCATCGC.....CAAGTCCCAGGAGCGAGT 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        651 yTyrLys...... 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    941 GCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTACGGCCCTAGCCCTGAG 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     891 CGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGG 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              635 lyLysArgAlaPro.SerProGlyAlaTyrLysThrAlaThrProProGl 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             841 ATCTACGAGACCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACAT 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    618 SerSerProAlaGlyTyrLysThrAlaSer......627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                803 .....TCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGT 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          759 CCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACA..... 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             584 rProSerGlnGlyProGlnGlyAlaProTyrProPheProProValProT 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     724 ACCACCCACCAGACCT......CCTTGGAGCTCTTCATGTA 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              674 TCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATGGC 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        555 GlnAlaGlyProAsn..GlyProProValSerSerSerSerAsnSerSer 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      627 GACCCAGGACCCAAAGCCCCCGA...ACACCCCCTGACATTCTCCGAGA 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              580 ATCCTGGAGAACCCCAA...GAACCAAGCGCCTCCAGGTCTCTACACGAA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               521 sAlaHisProTyrAlaMetSerProSerLeuGlySerLeuArgProTyrP 538
```

ATAN US/08/660, N-1996 6 1996 6 1996 6 1996 6 1997 747 1997 1999 9 1999
TYPE: Floppy disk SR: IBM PC compatible ING SYSTEM: PC-DOS/MS-DOS NB: Patentln Release #1 0 Version #1 2
₹ . .
; ZIP: 20005

```
169 AsnProThrSerProArgGlySerSerThrProTrpAlaThrAlaSerAr 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 rgLeuIleProArg...ProAlaLeuCysProTrpSerCysLeuArgArg 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497 ....AACACGGGATTCCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCAT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 TCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGC.. 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543 GGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACC 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 gLeuGlnProSerTrpProSerSerSerTrpSerLeuSerGlyGly.... 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         678 GTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATGGCACCA 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        632 ....AGGACCCAGCCAAAGCCCCCAACACCCCTGACATTCTCGAGATCGA 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||| ::::::||| |||::: :::||| |||
215 ProLeuSerSerArgArgGlnLeuCysSerArgThrProProSerPheTh 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 ......SerThrAlaProGlyThrThrSerThrProSerCysSerPro 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 ProLeuIleSerArgProProThrSerAlaGlyCysTrpGlnLysLeuCy 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 lyTrpPheSerLeuProGlyGlyPheLeuCysSerSerProAlaCysGly 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        770 ......TCGCGGGCAAGCATGGCG 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 sThrProAlaSerProProHisCysProAlaGlnGlyGlySerSerGlyG 283
                                                                                                                                           1039 GGGAAAGTGCAGGTGTCCGTCCTCAAGGGCC.....AGGTGTA 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          838 GGTATCTACGAGACCC......CAGCAGGCACCATCC...... 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 Trp.....valAlaSerTrpProLeuLysMetLeuArgAlaGlyThrTr 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         788 TGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGA 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 euLeuGlyThrLeuGlyPhePheSerIleLeuSerValSerCysGlyAsn 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 pThrThrAlaProProThrGlyGlySerSerLysAspProSerSerSerL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 TrpSerGlnLeuArgAlaAlaSerThrProSerLeuSerThrGlyValSe 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           869 TTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGG..... 913
                                               1077 CATCCTCGGCC 1087
                                                                                                                                                                                                                                                                                                                                                                                             364 rLeuSerGlnArgPheSerSerPheArgCysLeuGluSerThrMetSerP 381
                                                                                         401 .....AlaLeuSerArgAlaSerLeuLeuLeuSerCysT 412
                                                                                                                                                                                          391 ......TrpThrSerAlaSerProAsnTrpAspTrp.. 400
                                                                                                                                                                                                                                            989 AGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAA 1038
                                                                                                                                                                                                                                                                                         381 heSer......ThrSerCysLeuThrValLeuGly...... 390
                                                                                                                                                                                                                                                                                                                                           939 GGGCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTG 988
412 hrAlaserser 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCC.....ACCAGACCTCCT........rggAGCTCTTCATG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGTGCGCAAAATCAAACAAGGCCT 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....CysAlaArgLeuLeuPro 249
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-413-814-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT ; ORGANISM: Sorangium cellulosum US-09-413-814-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence 78, Application US/09413814 patent No. 6225064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-09-413-814-78 from: 1 to: 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-775-693-1 x US-09-413-814-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or TITLE OF INVENTION: heteropolyketide compounds FILE REFERENCE: PCT/US 99/23535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/413,814 CURRENT FILING DATE: 1999-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mueller, Joachim APPLICANT: Reichenbach, Hans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 CCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 .....SerProArgArgArgProSerProSerAlaArgSerProAlaI 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 AAGCTTGGGGCCA...AAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTT 203
                                                                                                                                                                                                                                                                                                                                                                                             387 leTrpGluArgProProArgArgProArgAspArgArgProArgAeu 403
                                                                                                                                                                                                                                                                                                                                                                                                                                     204 TGTGGAGGAGTTCATCTGGCCGGCCATCCAGT.....CCAGCGCACTGT 247
                                                                                                                                                                                                                                                                                                     404 LeuArgProAlaArgArgLeuAlaArgArgAspProGlyAspValProAs 420
                                                                                                                                                                                                                                                                                                                                               248 ATGAGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGC......CCTGC 291
                                         450 AlaProArgArgGly......AlaAlaAlaArg.ValProProAspA 463
                                                                                   368 ACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATA 417
                                                                                                                             437 laAspGlyArgGly......AlaArgGlyProGlyArgArgArg 449
                                                                                                                                                                       323 .....GGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGA 367
                                                                                                                                                                                                                 420 pProArgAlaAlaArgArgArgAlaProAlaAlaGlyAlaLeuProGlyA 437
                                                                                                                                                                                                                                                             418 AAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brandt, Petra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bloecker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bristol-Myers Squibb, Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gesellschaft fuer Biotechnologische Forschung mbH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cino, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beyer, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134.00 Length: 433
0.784 Gaps: 24
39.492 Percent Identity: 25.173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helmut
```

– ¥ ω	se		: 34 : 1 : 24.49	<pre></pre>	EQUENCE CHARACTERISTICS: LENGTH: 355 amino acids TYPE: amino acid	TELERA: 312/4/4-0448 TELEX: 25-3856 ORMATION FOR SEQ ID NO: 41	NUMBER: 2 NFORMATION 74-6300	NAME: Zeller, James P. REGISTRATION NUMBER: 28,49	APPLICATION N FILING DATE:	APPI FIL] IOR	NOMBER: US/08/483,53 : 07-MAR-95 ION: 514 FION DATA.	FTWARE: PatentIn Release #1.0, ENT APPLICATION DATA:	COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DC	MEDIUM TYPE: Flore 44ct	STATE: Illinois COUNTRY: United States of America	ADDRESSEE: Marshall, O'Toole, Gerstein, N STREET: 6300 Sears Tower, 233 South Wacke	TITLE OF INVENTION: MELHOG FOR Treat NUMBER OF SEQUENCES: 43 CORRESPONDENCE ADDRESS:	APPLICANT: Roizman, Bernard APPLICANT: Chou, Joany	q_documen Sequence Patent No GENERAL	<pre>seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:US-08-483-533-41</pre>	704ProProAspGlnGly 708
	82	gn seg 1/1 to: US-08-483-533-41 from: 1 to: 355 206 TGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGAC 25 ::: 82 TTPProAspSerProProProGluSerAlaPrOGluAlaAr 95	<pre>gnment_block: -09-775-693-1 x US-08-483-533-41 ign seg 1/1 to: US-08-483-533-41 from: 1 to: 355 206 TGGAGGAGTTCATCTGGCCGGCCATCCAGCTCCAGCGCACTGTATGAGGAC 25 </pre>	gnment_scores: Quality: 131.50 Ratio: 1.035 rcent Similarity: 37.026 percent Identity: 24.490 gnment_block: -09-775-693-1 x US-08-483-533-41 ign seg 1/1 to: US-08-483-533-41 from: 1 to: 355 206 TGGAGGAGTTCATCTGGCCGGCCATCCAGCGCACTGTATGAGGAC 25 ::	TOPOLOGY: linear protein MOLECULE TYPE: protein MOLECULE TYPE: protein 08-483-533-41 gnment_scores: Quality: 131.50 Ratio: 1.035 rcent Similarity: 37.026 Percent Identity: 24.490 gnment_block: -09-775-693-1 x US-08-483-533-41 ign seg 1/1 to: US-08-483-533-41 ign seg 1/1 to: US-08-483-533-41 from: 1 to: 355 206 TGGAGGAGTTCATCTGGCCGGCCATCCAGCGCACTGTATGAGGAC 25	SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein 08-483-533-41 gnment_scores: Quality: 131.50 Ratio: 1.035 rcent Similarity: 37.026 Percent Identity: 24.490 gnment_block: -09-775-693-1 x US-08-483-533-41 ign seg 1/1 to: US-08-483-533-41	INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein 08-483-533-41 Quality: 131.50 Ratio: 1.035 rcent Similarity: 37.026 Percent Identity: 24.490 gnment_block: -09-775-693-1 x US-08-483-533-41 ign seg 1/1 to: US-08-483-533-41 ign seg 1/1 to: US-08-483-533-41 ign seg 1/1 to: US-08-483-533-41	REFERENCE/DOCKET NUMBER: 28097/32742 TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300 TELEPHONE: 312/474-0448 TELEX: 312/474-0448 TELEX: 25-3856 INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein 08-483-533-41 Length: 343 Freent Similarity: 131.50 Ratio: 1.035 Ratio: 1.035 Ratio: 1.035 Percent Identity: 24.490 9JUNENT_Block: -09-775-693-1 x US-08-483-533-41 ign seg 1/1 to: US-08-483-533-41	REGISTRATION NUMBER: 28,491 REFERENCE/DOCKET NUMBER: 28,491 RELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-0448 TELEX: 25-3856 INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids STRANDEDNESS: single MOLECULE TYPE: protein 08-483-533-41 9nment_scores: Quality: 131.50 Ratio: 1.035 Ratio: 1.035 Ratio: 1.035 Reference Percent Identity: 24.490 9nment_block: -09-775-693-1 x US-08-483-533-41 ign seg 1/1 to: MS-08-483-533-41	APPLICATION NUMBER: 07/861,233 ATTORNEY/AGENT INFORMATION: NAME: Zeller, James P. REGISTRATION NUMBER: 28,491 REFERENCE/DOKET NUMBER: 28097/32742 TELECOMMUNICATION INFORMATION: TELEFAX: 312/474-6300 TELEFAX: 312/474-0448 TELEFAX: 355 amino acids TYPE: amino acids STOPLOGY: linear MOLECULE TYPE: protein 08-483-533-41 gnment_scores: gnment_scores: gnment_scores: gnment_block: -09-775-693-1 x US-08-483-533-41 ign seg 1/1 to: US-08-483-533-41 from: 1 to: 355 206 TGGAGGAGGTTCATCTGGCCGGCCATCCAGCGCACTGTATGAGGAC 25	APPLICATION NUMBER: 08/419,853 PRIOR APPLICATION DATE: 11-APR-95 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 07/861,233 PRIOR APPLICATION NUMBER: 07/861,233 PRIOR APPLICATION NUMBER: 28,491 REFERENCE/DOCKET NUMBER: 28,491	PILING DATE: 07-MAR-95 PILING DATE: 11-APR-95 PRIOR APPLICATION NUMBER: 08/419,853 PRIOR APPLICATION NUMBER: 08/419,853 PRIOR APPLICATION NUMBER: 07/861,233 PRIOR APPLICATION NUMBER: 07/861,233 PRIOR APPLICATION NUMBER: 07/861,233 PRIOR APPLICATION NUMBER: 28,491 REFERENCE/DOCKET NUMBER: 28097/32742 PRESISTRATION NUMBER: 28,491 REFERENCE/DOCKET NUMBER: 28097/32742 PRESISTRATION OR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids STYPE: mino acids STYPE: mino acid STRANDEDNESS: single MOLECULE TYPE: protein 08-483-533-41 SOUBLITY: 131.50 Caps: 19 OB-483-533-41 SOUBLITY: 131.50 Caps: 19 OB-483-533-41 SOUBLITY: 37.026 Percent Identity: 24.490 9nment_block: 105-08-483-533-41 19 19 19 19 19 19 206 TGGAGAGAGTTCATCTGGCCGGCCATCCAGCGCACTGTATGAGGAC 25 1	CURRENT APPLICATION NATA: APPLICATION NUMBER: US/08/483/533 FILING DATE: 07-MAR-95 CLASSIFICATION NUMBER: US/08/483/533 FILING DATE: 11-APR-95 CLASSIFICATION NUMBER: 08/419,853 FILING DATE: 11-APR-95 PRICATION NUMBER: 07/861,233 FILING DATE: 11-APR-95 PRICATION NUMBER: 07/861,233 PRICATION NUMBER: 07/861,233 PRICATION NUMBER: 28/491 REGISTRATION NUMBER: 28/491 REGISTRATION NUMBER: 28/491 REGISTRATION INFORMATION: NAME: Zeller, James P. REGISTRATION INFORMATION: REGISTRATION INFORMATION: TELEPHONE: 312/474-0448 TELEPHONE: 312/474-0448 TELEPHONE: 312/474-0448 TELEPHONE: 355 amino acids TYPE: amino acids TYPE: amino acid STOPLLOGY: linear TYPE: mino acid STYPE: min	COMPUTER: IBM PC COMPATIBLE COMPETATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION UNMBER: US/08/483,533 CLASSIFICATION: 514 PRIOR APPLICATION: 514 PRIOR APPLICATION: 514 PRIOR APPLICATION: 514 PRIOR APPLICATION UNMBER: 08/419,853 FILING DATE: 11-APR-95 PRIOR APPLICATION DATA: APPLICATION UNMBER: 07/861,233 FILING DATE: 31-MAR-92 PRIOR APPLICATION NOMBER: 28,491 REFIGENCE/DOCKET NUMBER: 28,491 REFIGENCE/DOCKET NUMBER: 28097/32742 TELECOMMUNICATION INFORMATION: NAME: Zeller, James P. REGISTRATION NUMBER: 28097/32742 TELEFAX: 312/474-0448 TELEX: 25-3856 INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS: LENGTH: 355 anino acids TELEX: 25-3856 INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS: LENGTH: 355 anino acids STRANDEDNESS: single MOLECULE TYPE: anino acid STRANDENESS: single MOLECULE TYPE: protein 08-483-533-41 19nment_Scores: Quality: 131.50 Ratio: 1.035 Percent Similarity: 37.026 Percent Identity: 24.490 gnment_block: -09-775-693-1 x US-08-483-533-41 from: 1 to: 355 206 TGGAGGAGGTTCATCTGGCCGGCCATCCAGCGCACTGTATGAGGAC 25 1 ::: 82 TTPPTOASPSEPPTOPTOPTOGGLUSCATCCAGCGCACTGTATGAGGAC 25	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOSTWARE: PatentIn Release #1.0, Version #1.25 SOSTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/483,533 CLASSIFICATION DATA: APPLICATION NUMBER: US/08/483,533 CLASSIFICATION NUMBER: 07/861,233 FILING DATE: 11-APR-95 PRIOR APPLICATION NUMBER: 28,491 REPERENCE/DOCKET NUMBER: 28,491 REPERENCE/DOCKET NUMBER: 28097/32742 TELECOMMUNICATION INFORMATION: NAME: Zeller, James P. REFERENCE/DOCKET NUMBER: 28097/32742 TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300 TELEFAX: 312/474-6300 TELEFAX: 312/474-6300 TELEFAX: 312/474-6300 TELEPHONE: 315 mnino acids STRANDEDWESS: Single TOPOLOGY: linear TOPOLOGY: 131.50 TRANDEDWESS: 10.05 SEQUENCE TYPE: protein 08-483-533-41 19 gnment_scores: Quality: 131.50	STRIE: Illinois COUNTRY: Office States of America ZIP: 60606-6402 COMPUTER COMPOSTATION OF AMERICA MEDIUM TYPE: Floppy disk COMPUTER EADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPOSTATION COMPUTER: ILL COMPOSTATION COMPUTER: ILL COMPOSTATION	ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Bor STREE: 6300 Sears Tower, 233 South Wacker Drive CTTY: Chicago STATE: Illinois COUNTRY: United States of America COUNTRY: United States #1.0, Version #1.25 ADDIUM TYPE: FLOPPY disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: 18M PC COMPATA: US/08/483,533 FILING DATE: 11-AR-95 FILING DATE: 31-AR-92 FIL	CORRESPONDENCE ADDRESS: ADDRESSE: MAISHAIL, O'TOOLE, GETSTEIN, MUTTAY & BOT STRUETCHESSEE: MAISHAIL, O'TOOLE, GETSTEIN, MUTTAY & BOT STREET: 6300 Sears Tower, 233 South Wacker Drive STREET: 6300 Sears Tower, 233 South Wacker Drive COUNTRY: Chicago STATE: Illinois COUNTRY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 APPLICATION NUMBER: US/08/483,533 CLASSIFICATION ADTA: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/419,853 ETLING DATE: 11-APR-95 PRIOR APPLICATION NUMBER: 07/861,233 APPLICATION NUMBER: 28/491 FRIENDED ADTE: 31-MAR-92 APPLICATION NUMBER: 28/491 FRIENDED ADTE: 31-MAR-92 APPLICATION NUMBER: 28/491 REFERENCE/DOCKET NUMBER: 28/97/32742 TELEPHONE: 312/474-3300 TELEFAX: 312/474-300 TELEFAX: 312/474-300 TELEFAX: 312/474-300 TELEFAX: 312/474-300 TELEFAX: 312/474-300 TELEFOMMUNICATION FORMATION: MAME: CHARACTERISTICS: ENGURNE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids STRANDENESS: Single MUNDRASS: Single MUNDRASS: SINGle TYPE: amino acid STRANDENESS: SINGle TOPOLOGY: Innear MOLECULE TYPE: protein 08-483-533-41 10-483-533-41 10-483-533-41 10-89-775-693-1 x US-08-483-533-41 10-97-775-693-1 x US-08-483-533-41 10-11:::11 10-11::11 10-	APPLICANT: Chou, Joany TITLE OF INVENTION: Method for Treating Tumorigenic NUMBER OF INVENTION: Diseases CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Bor STRIE: Illinois STRIE: Illinois COUNTRY: United States of America COMPUTER READDRALE FORM: MEDIUM TYPE: Hidden OPERATING SYSTEM: PC-COMPATIBLE OPERATION NUMBER: US/08/483,533 CUASSIFICATION INDRES: US/08/483,533 CUASSIFICATION NUMBER: US/08/483,533 FILING DATE: 11-ARR-95 CUASSIFICATION NUMBER: US/08/419,853 PRIOR APPLICATION US/08/419,853 PRIOR APPLICATION US/08/419,853 PRIOR APPLICATION US/08/41	Sequence 41, Application US/08483533 Patent No. 6172047 GENERAL INFORMATION: APPLICANT: Chou, Joany TITLE OF INVENTION: Method for Treating Tumorigenic NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSEE: MAISHALL, O'TOOLE, Gerstein, Murray & BOT STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois CONFUTER: Illinois CONFUTER: ILLInois CONFUTER: ILLINOis CONFUTER: ILLINOis CONFUTER: ILLINOis COMPUTER: IDBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: O'TOOLE, STATE LILING DATE: 07-MAR-95 CLASSIFICATION NUMBER: US/08/483,533 CLASSIFICATION NUMBER: US/08/483,533 FILING DATE: 31-MAR-95 PRIOR APPLICATION NUMBER: 08/419,853 FILING DATE: 31-MAR-95 PRIOR APPLICATION NUMBER: 28,491 FILING DATE: 31-MAR-95 PRIOR APPLICATION NUMBER: 31-MAR-95 PRIOR APPLICATION NUMBER: 31-MAR-95 PRIOR APPLICATION NUMBER: 31-MAR-95 PRIOR APPLIC	eeq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-483-533-4. *eq_accomentation_block: Sequence 41. Application US/08483533 Patant No. 6172047 Patant No. 6172042 Patant No. 6172043 Patant No. 6172042 Patant No. 61820 P
256 CGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGGCAAACA 305		gn seg 1/1 to: US-08-483-533-41 from: 1 to: 35	<pre>gnment_block: -09-775-693-1 x US-08-483-533-41 ign seg 1/1 to: US-08-483-533-41 from: 1 to: 355</pre>	9nment_scores: Quality: 131.50 Ratio: 1.035 recent Similarity: 37.026 percent Identity: 24.49 9nment_block: -09-775-693-1 x US-08-483-533-41 from: 1 to: 355	STRANEDNESS: single TOPOLOGY: linear TOPOLOGY: linear MOLECULE TYPE: protein 08-483-533-41 9nment_scores: Quality: 131.50 Ratio: 1.035 rcent Similarity: 37.026 percent Identity: 24.49 9nment_block: -09-775-693-1 x US-08-483-533-41 from: 1 to: 355	SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein 08-483-533-41 gnment_scores: Quality: 131.50 Quality: 1.035 rcent Similarity: 37.026 Percent Identity: 24.49 gnment_block: -09-775-693-1 x US-08-483-533-41 ign seg 1/1 to: US-08-483-533-41 from: 1 to: 355	INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS: LENGIH: 355 amino acids TYPE: amino acids STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein 08-483-533-41 gnment_scores: Quality: 131.50 Ratio: 1.035 recent Similarity: 37.026 percent Identity: 24.49 gnment_block: -09-775-693-1 x US-08-483-533-41 from: 1 to: 355	REFERENCE/DOCKET NUMBER: 28097/32742 TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-0300 TELEX: 25-3856 INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids TYPE: amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein 08-483-533-41 gnment_scores: Quality: 131.50 Ratio: 1.035 rcent Similarity: 37.026 Percent Identity: 24.49 gnment_block: -09-775-693-1 x US-08-483-533-41 from: 1 to: 355	REFERENCE/DOCKET NUMBER: 28,491 REFERENCE/DOCKET NUMBER: 28,474 REFERENCE/DOCKET NUMBER: 29,474 REFERENCE/DOCKET NUMBER: 29,474 REFERENCE/DOCKET NUMBER: 29,474 REFERENCE/DOCKET NUMBER: 29,474 REFERENCE/DOCKET NUMBER: 24,49 REFERENCE/DOCKET NUMBER: 28,491 REFERE	APPLICATION NUMBER: 07/861,233 FILING DATE: 31-MAR-92 ATTORNEY/AGENT INFORMATION: NAME: Zeller, James P. REGISTRATION NUMBER: 28.491 REFERENCE/DOCKET NUMBER: 28097/32742 TELEPHONE: 312/474-6300 TELEPHONE: 312/474-6448 TELEPHONE: 312/474-6448 TELEPHONE: 312/474-6430 TELEPHONE: 312/474-6430 TELEPHONE: 312/474-6430 TELEFAX: 32-3856 INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERRISTICS: LENGTH: 355 amino acids TYPE: amino acid STRANDEDWESS: Single MOLECULE TYPE: protein 08-483-533-41 9nment_scores: Quality: 131.50 Ratio: 1.035 Ratio: 1.035 Retio: 1.035 reent Similarity: 37.026 Percent Identity: 24.49 9nment_block: -09-775-693-1 x US-08-483-533-41 from: 1 to: 355	APPLICATION NUMBER: 08/419,853 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 07/861,233 FILING DATE: 31-MAR-92 ATTORNEY/AGENT INFORMATION: NAME: Zeller, James P. REGISTRATION NUMBER: 28.491 REFERENCE/DOCKET NUMBER: 28.997/32742 TELECOMMUNICATION INFORMATION: TELEFAX: 312/474-6448 TELEFHONE: 312/474-630 TELEFAX: 325-3856 INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids TYPE: amino acids STRANDEDNESS: single TOPOLOGY: linear TOPOLOGY: linear TOPOLOGY: linear TOPOLOGY: linear TOPOLOGY: linear TOPOLOGY: 131.50 Ratio: 1.035 Ratio: 1.035 Resent Similarity: 37.026 Percent Identity: 24.49 gnment_block: -09-775-693-1 x US-08-483-533-41 from: 1 to: 355	FILING DATE: 07-MAR-95 PILING DATE: 07-MAR-95 APPLICATION NUMBER: 08/419,853 FILING DATE: 11-APR-95 PILING DATE: 11-APR-95 PILING DATE: 11-APR-95 PILING DATE: 31-MAR-92 APPLICATION NUMBER: 07/861,233 APPLICATION NUMBER: 28.491 REFIRENCE, DOCKER INVAMER: 28097/32742 TELEPHONE: 312/474-6300 TELEPHONE: 312/474-6300 TELEPHONE: 312/474-6300 TELEPHONE: 312/474-6448 TELEPHONE: 312/474-6300 TELEPHONE: 312/474-6	CURRENT APPLICATION NUMBER: US/08/483,533 FILING DATE: 07-MAR-95 CLASSIFICATION NUMBER: US/08/483,533 FILING DATE: 07-MAR-95 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/419,853 FILING DATE: 11-APR-95 PRIOR APPLICATION NUMBER: 07/861,233 FILING DATE: 11-APR-95 PRIOR APPLICATION NUMBER: 28,491 FILING DATE: 31-MAR-92 APPLICATION NUMBER: 28,491 REGISTRATION NUMBER: 28097/32742 REGISTRATION NUMBER: 28097/32742 TELEPHONE: 312/474-6300 TELEFAX: 312/474-6300 TELEFAX: 312/474-630 TELEFAX: 312/474-630 TELEFAX: 312/474-630 TELEFAX: 355 amino acids STEALMOEDNESS: single MOLECULE TYPE: protein MOLECULE TYPE: protein 08-483-533-41 STRANDEDNESS: Single MOLECULE TYPE: protein 08-483-533-41 STRANDEDNESS: Single MOLECULE TYPE: protein 08-483-533-41 STRANDEDNESS: Single TOPOLOGY: linear MOLECULE TYPE: protein 08-483-533-41 Length: 34 Treent Similarity: 37.026 Percent Identity: 24.49 gnment_block: -09-775-693-1 x US-08-483-533-41 from: 1 to: 355	COMPUTER: IBM PC COMPATIBLE COMPATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.2 APPLICATION NUMBER: US/08/483,533 FILING DATE: 07-MAR-95 CLASSIFICATION: 514 PRIOR APPLICATION NUMBER: 08/419,853 FILING DATE: 11-APR-95 FILING DATE: 11-APR-95 FILING DATE: 11-APR-95 FILING DATE: 11-APR-95 FILING DATE: 31-MAR-95 FILING DA	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.2 CURRENT APPLICATION DATA: APPLICATION UNUMBER: US/08/483,533 FLING DATE: 07-MAR-95 PRIOR APPLICATION UNUMBER: US/08/483,533 FLING DATE: 11-APR-95 PRIOR APPLICATION UNUMBER: 07/861,233 APPLICATION NUMBER: 07/861,233 PRIOR APPLICATION NUMBER: 28,491 REPLICATION NUMBER: 28,491 REFERENCE/DOCKET NUMBER: 24,491 REFERENCE/DOCKE	STATE: Illinois COUNTRY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.2 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/483,533 FILING DATE: 07-MAR-95 CLASSIFICATION NUMBER: U8/08/483,533 FILING DATE: 11-APR-95 FILING DATE: 11-APR-95 FILING DATE: 31-MAR-92 APPLICATION NUMBER: 28,491 REFINENCE/DOCKET NUMBER: 28097/32742 FILING DATE: 312/474-6448 FILECOMMUNICATION INFORMATION: NAME: 26-18er: 12/474-6300 FILEFAX: 312/474-6448 TELEFAX: 312/474-6448 TELEFAX: 355 amino acids SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids STRANDEDNESS: single MOLECULE TYPE: protein MOLECULE TYPE:	ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Bor STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: United States of America COUNTRY: United States of America COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: LBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 APPLICATION NUMBER: US/08/483,533 FILING DATE: 07-MAR-95 CURRENT APPLICATION NUMBER: 08/419,853 FILING DATE: 07-MAR-95 CUASSIFICATION NUMBER: 08/419,853 FILING DATE: 11-APR-95 PRIOR APPLICATION NUMBER: 28/419,853 PRIOR APPLICATION NUMBER: 28/491 FILING DATE: 31-MAR-92 PRIOR APPLICATION NUMBER: 28/491 FILING DATE: 31-MAR-92 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 28/491 FILING DATE: 31-MAR-92 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 28/491 FILECOMMUNICATION INFORMATION: REGISTRATION NUMBER: 28/491 FILECOMMUNICATION INFORMATION: TELEPHONE: 312/474-0448 TELECOMMUNICATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids STYPE: mino	CORRESPONDENCE ADDRESS: ADDRESSE: A3 CORRESPONDENCE ADDRESS: ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Bor STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STREET: 111inois COUNTYR: United States of America ZIP: 60606-6402 ZIP: 60606-6402 ZIP: 60606-6402 ZIP: 60606-6402 COMPUTER: IBM PC COMPATION MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIOLE COMPUTER: IBM PC COMPATIOLE COMPUTER: IBM PC COMPATIOLE SOFTWARE: PATENTIN SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN DATA: APPLICATION NUMBER: US/08/483,533 CLASSIFICATION: 514 PRIOR APPLICATION NUMBER: US/08/483,533 FILING DATE: 11-APR-95 CLASSIFICATION NUMBER: 07/861,233 FILING DATE: 11-APR-95 FILING DATE: 11-APR-95 FILING DATE: 11-APR-95 FILING DATE: 31-ARR-92 FILING DATE: 31-ARR-92 FILING DATE: 31-ARR-92 FILING DATE: 31-ARR-92 FILING DATE: 31-ARR-93 FILING DATE: 31-ARR-93 FILING DATE: 31-ARR-95 FILIN	APPLICANT: Chou, Joany TITLE OF INVENTION: Method for Treating Tumorigenic NUMBER OF INVENTION: Diseases CORRESPONDENCE ADDRESS: ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Bor STREET: 6300 Sears Tower, 233 South Wacker Drive STREET: 111inois COUNTRY: United States of America COUNTRY: United States of America COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: DATE: O'T-OSC/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 ELIKE DATE: O'T-WAR-95 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/483,533 CLASSIFICATION DATA: APPLICATION NUMBER: 00/419/853 FILING DATE: O'T-WAR-95 CLASSIFICATION NUMBER: 07/861,233 APPLICATION NUMBER: 08/419/853 FILING DATE: 11-APR-95 PRIOR APPLICATION NUMBER: 28/491 FRIDRESTATION NUMBER: 28/491 FRIDRESTATION NUMBER: 28/491 REFERENCE/DOCKET NUMBER: 28/491 REFERENCE/DOCKET NUMBER: 28/491 RELECOMMUNICATION INFORMATION: NAME: 2611er, James P. REGISTRATION OF SEQ ID NO: 41: SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids STRANDENESS: single MOLECULE TYPE: protein 08-483-533-41 19nment_Scores: QUALITY: 131.50 Length: 343 rcent Similarity: 37.026 Percent Identity: 24.490 gnment_block: 09-775-693-1 x US-08-483-533-41 Ign seg 1/1 to: US-08-483-533-41 Ign seg 1/1 to: US-08-483-533-41	Sequence 41. Application US/08483533 Patent No. 6172047 Patent No. 6172047: Roizman, Bernard APPLICANT: Roizman, Bernard APPLICANT: Chou, Joany TITLE OF INVENTION: Method for Treating Tumorigenic TITLE OF INVENTION: Diseases CORRESPONDENCE ADDRESS: 4 CORRESPONDENCE ADDRESS: 4 CONTRESSEE: Marishall, O'Toole, Gerstein, Murray & Bor STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois CONPUTER READABLE FORM: MEDIUM TYPE: Hoppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Hoppy disk COMPUTER: LBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 APPLICATION NUMBER: US/08/483,533 FILING DATE: 07-MAR-95 APPLICATION NUMBER: 08/419,853 FILING DATE: 11-APR-95 APPLICATION NUMBER: 08/419,853 FRILING DATE: 31-APR-95 APPLICATION NUMBER: 28/491 PRIOR APPLICATION NUMBER: 28/491 PRIOR APPLICATION NUMBER: 28/991 REFERENCE/DOCKET NUMBER: 28/997/32742 TELEFONMUNICATION INFORMATION: NAME: 26ller, James P. REGISTRATION UNMBER: 28/997/32742 TELEFONMUNICATION INFORMATION: NAME: 26ller, James P. REFERENCE/DOCKET NUMBER: 28/997/32742 TELEFONMUNICATION INFORMATION: NAME: 26ller, James P. REFERENCE/DOCKET NUMBER: 28/997/32742 TELEFONMUNICATION INFORMATION: NAME: 26ller, James P. REFERENCE/DOCKET NUMBER: 28/997/32742 TELEFONMUNICATION INFORMATION: SEQUENCE CHARACTERISTICS: TYPE: maino acid STRANDEDNESS: single NOLECULE TYPE: protein 08-483-533-41 19 19 108-483-533-41 19 19 19 19 109-775-693-1 x US-08-483-533-41 109 199-775-693-1 x US-08-483-533-41 109 199-775-693-1 x US-08-483-533-41 100 101 101 102 103 104 105 105 106 107 108 108 109 107 108 108 109 109 109 109 109 109	eeq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-483-533-4. eeq_documentation_block: eeq_docume

	GCGGGAGTCCCCACTGTCTCTACAA 1112 ::: ProGlyMetVallleLysAsnLeuGln 346	338 338
ω ω	:::	Ñ
10		1059
32	::: ::: ::: gGlnArgGlyGlyAlaArgProThrSerValArgArgValPheGlyAl	305
10	GAAAGTGCAGGTGTCCGT	1040
30	SerGlnGlyGlyProProArgGlyArgAspTrpProIleGlyGlyAr	290
10	TGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGG	990
28	uArgArgTrpGlnGluProArgIleTyrThrLeuGlyAlaSerProPr	7
98	AATTTGCTGAGCTGGTGTATACCGGTTTTACGGCCTAGCC	940
27	AlaProGlySerSer	259
93	GAGGCCTTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTG	890
25	ro	245
88	GAGACCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACA	840
24	ArgProValProGlyProTrpProAlaGluProAla	231
83	GCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGG	790
23	ArgArgProArgArgSerSerGlyArgAlaTrpG	215
78	CCTGAACGAAGTCGCGGGCAAGCATGGCGTG	759
21	gGlyProAlaSerGlyProThrGlyLeuGlySe	199
75	GAGCTCTTCATGTA	744
199	oThrSerGlyCysAlaThrTrpTrpSerGlyProArgProProAlaT	183
74	CAACGTCAAGGATGGCACCACCCACCAGACCTCCTT	706
18:	ProArgProProArgGlyCysAlaSerArg	172
705	CCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGAAGGTG	656
17	gSerProProArgProProArgProProArgProProArg	158
655	CGAAGACCCAGGACCCAGCCAAAGCCCCCAACA	606
158	aArgAlaGlyArgGlyArgA	148
909	GCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGC	556
148	ProArgSerThrTrpAr	140
555	GTGGAGCATGGATGAGAACCTC	506
139		139
505	CCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGA	456
139	.ProSerAlaPheArgAlaSerProSerAlaCysAlaSer 1	126
\$ 5 5	CCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAA	406
125	ArgAla 1	124
405	CAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTG 4	356
1	TrpAlaArgGlyAlaGlyLeuThrProProfinerovro	111

```
seq_documentation_block:
    Sequence 3, Application PC/TUS9106532
    GENERAL INFERMATION:
    APPLICANT: Roizman, Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:PCT-US91-06532-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
us-09-775-693-1 x PCT-US91-06532-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US91-06532-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 2737:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/346-5750
TELEPAX: 312/984-9740
TELEFAX: 312/984-9740
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: PCT-US91-06532-3 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: RETITLE OF INVENTION: Valuabler of SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: AMINO ACID TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                  111 ...TrpAlaArgGlyAlaGlyLeuThrPro......ProThrProPro 123
                                                                                                                                                                                                                                                                                                                                                                                                                      206 TGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGAC 255
  126
                                              406 GCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAA 455
                                                                                     124 ArgAla..... 125
                                                                                                                                                                                                                              306 AGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCA 355
                                                                                                                                                                                                                                                                                                                              256 CGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACA 305
                                                                                                                                         356 CAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTG 405
                                                                                                                                                                                                                                                                               82 TrpProAspSerProProProGluSerAlaProGlu......AlaAr 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Two Firs
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US91/06532
FILING DATE: 19910910
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 60603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
.ProSerAlaPheArgArgAlaSerProSerAlaCysAlaSer..... 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Two First National Plaza Suite 2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131.50
1.035
37.026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant Herpes Simplex Viruses Vaccines and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 24.490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27373/8235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 355
```

	<pre>seq_documentation_block: ; Sequence 72, Application US/08642255 ; Patent No. 5773249 ; GENERAL INFORMATION: APPLICANT: CAPPELLO, Joseph ; APPLICANT: FERRARI, Franco A.</pre>
	<pre>seq_name: /cgn2_6/ptodata/2/laa/5A_COMB.pep:US-08-642-255-72</pre>
	1086 CCGGGAGTCCCCACTCTCTCTCTACAA 1112 ::: 338 ProGlyMetValIleLysAsnLeuGln 346
ω	::: :::
1085	AAGGGCCAGGTGTACATCCTCGG
1058 322	1040 GGAAAGTGCAGGTGTCCGT
305	290 SerGlnGlyGlyProProArgGlyArgAspTrpProIleGlyGlyAr
1039	AGTCCCAGGAGCGAGTGGAAG
289	::: rLeuGlyAlaSerProPro
989	AAATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGA
939 273	890 TCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTG
U C	45ArgArgThrArgSerAsnValThrProGluAlaAlaTrpValPh
œ	GAGACCCCAGCAGCACCATCCTTTACCATGCTCATTTACAC
839 244	790 GGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGG
789 231	759
215	99 rpArgAlaA
758	4 GGAGCTCTTCATGTA
743 199	706 ACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTT
182	 roArgProProAr
705	TCTCGAGATCGAGTTCAAAAAA
655 171	606 GCCTCCAGGTCTCTACACGAAGACCCAAGACCCAAGCCCAAAGCCCCCAACA
158	148 aCysAspAlaArgAlaGlyArgGlyArgA
4	.40ProArgSerThrTrpArgAlaCysA
(JI	TTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCT
139	139
505	456 CCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGA

```
; TYPE: amino acid
; STRANDENNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: prote
US-08-642-255-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block: US-09-775-693-1 x US-08-642-255-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-642-255-72 from: 1 to: 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 amino acids
TYPE: amino acid
371 ATCAGGTCCGGTTTGAGCTCAGCTGCTACTCGCCCCCCAGATAAAG 420
                                                                355 lyProProGlyAlaGlnGlyProAlaGlyProGlyGlySerArgGlyAsp 371
                                                                                                         330 GGCCA.....AGTATGTGTCCCACGGCGCCA...CAGGAAAGGGGAACG 370
                                                                                                                                                         338 oProGlyAlaGlnGlyProAlaGlyProGlyGlySerArgGlyAspProG 355
                                                                                                                                                                                                                                                     322 GlyAlaGlnGlyProAlaGlyProGlyGlySerArgGlyAspProGlyPr 338
                                                                                                                                                                                                                                                                                             305 laGlnGlyProAlaGlyProGlyGlySerArgGlyAspProGlyProPro 321
                                                                                                                                                                                                         280 GCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCCCAGCGGGAGGG 329
                                                                                                                                                                                                                                                                                                                                                                                              193 AGCAGGGAGTTTGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 GlyAlaHisGlyProAlaGlyPro...LysGlyAlaHisGlyProAla.. 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/642,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 GGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGAAGCCAC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: A55556-3/BIR TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 494-8700
TELEPHONE: (415) 494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: High Molecular Weight Collagen-Like TITLE OF INVENTION: Protein Polymers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
CITY: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           .........GlyProLysGlyAlaHisGlyProAlaGlyProLysGlyA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           San Francisco
: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130.00
0.818
40.050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 397
Gaps: 27
Percent Identity: 28.463
```

C. Park

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-945-283-2
seq_documentation_block:

517 365	468 CCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCCATCCCGG	
467 348	421 GTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGG ::: ::::::::::::::::::::::::::::::	
	371 ATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAG :::: 335 sGlnGlyProProThrSerPro	
ı w		
370	21 GCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGG	
320 321	271 ACCTCTCTTGCCAGGCCCTGCATCGCCGCAAACAAGTGGAAATCGCCCA	
0		
270	seg 1/1 to: US-07-945-283-2 from:	
	alignment_block: US-09-775-693-1 x US-07-945-283-2	
	Qua R Percent Simila	
	D D	
	; TOPOLOGY: LINEAR ; MOLECULE TYPE: protein US-07-945-283-2	
	LENGTH: 1958 amino a	
	A: 309-003-4120 N FOR SEQ ID NO: CHARACTERISTICS	
	ECOMMUNICATION INF ELEPHONE: 309-685	
	NAME: Ribando, Curtis P REGISTRATION NUMBER: 27976	
	CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATIO	
	APPLICATION NUMBER: UFILING DATE: 19920911	
	SOFTWARE: PatentIn Release # CURRENT APPLICATION DATA:	
	COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DO	
	COMPUTER READABLE I	
	STATE: COUNTRY	
	STREET: 1815 No. 5352596t CITY: Peoria	
	PONDENCE ADDRESS: ESSEE: Curtis P. Ribando	
	TITLE OF INVENTION: FSEUDOLOUSES VILLE FOR THE SECTION OF INVOLVING THE EPO and LLT Genes	
•	APPLICANT: Cheung, Andrew A. APPLICANT: Wesley, Ronald D. APPLICANT: Wesley, Ronald D. APPLICANT: Wesley, Ronald D.	
	. 5352596 INFORMATION:	
	2, Appl	

	TCAGGCTGAAGGAATATCATCGTCTC	1190
2	SerGluSerGluSerSe 59	8
89	GGGTGATTATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCC 11	4
б	GlyAlaGlyGluSerGlu 58	581
39	GAGTCCCCACTGTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCA 11	1090
0 9	:::::::	95
0 0	GGAAAGTGCAGGTGTCCGTCCTAAAGGGCAAAAGTGTGATGATGATGAAGAGAAAAG	4
39	GluAspGluAspGluAspGluAspGluAspArgalaGluAspGluAspGluAspGluAspGluAspGluAspGluAspGluAspGluAspGluAspArgalaGluAspGluAspGluAspArgalaGluAspGluAspArgalaGluAspGluAspArgala	1032
1	rgArgAlaGluGlyThrGluAlaAlaAlaAlaAspAlaGluGluGlu 55	w
31	ATCGCCAAGTCCCAGGAGCG	1012
СI	LysA 5	534
	TGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGC 1	962
	ProGlyArgGlyGlyArgArgGlyGly5	524
Ē	GGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGC	912
ŭ i	roAlaGlyGlySerAlaArgArgArgArgArgGlyGlyGlyGlyGlyPro 5	507
1	· · · · · · · · · · · · · · · · · · ·	876
)7		490
3	ATCCTTTACCA8	863
90	ArgAspAspProArgProProSerProProProArgPro	477
52	CTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAGCAGGCA 8	816
76	1/11::::::	6
л ,	AAGCATGGCGTGGGCCGTATTGACATCGTGGACAACCG 8	768
61	hrLeuPheSerHisSerGluAsnLysLeuPheSerHisProMetG 4	44.
67	7 7	76
44	roSer.ProGlnLysIleSerGluThrArgAlaGlySerGluAsnThrAl 4	428
67	3 CATGTACCTGAACGA 7	75
28	OSerThrArgProProProProGlnArgProProProArgTrpProProP 4	411
52	9 AACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTT 7	70
11	9 ProSerThrSerSerSerSerSerHisGlnGlyProPr 4	39
08	9 CTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGAAGGTGACC 7	65
86	3 HisHisGlnAspProProGlyGlyGlyProProSerProProArg 3	38
58	CGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCC 6	61
82	1ProGlyGlyProProSerThrSerSerHisHis 3	7
17	8 TACGAGGCTGGAATCCTCGAGAACCCCAAGAACCCCCTCCCCCCCC	56
70	::: 5 sHisHisGlnAspPro	36
567		51

;

```
alignment_block:
US-09-775-693-1 x US-08-735-041A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-735-041A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
   Sequence 2, Application US/08735041A
   Patent No. 5914251
                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-735-041A-2 from: 1 to: 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-735-041A-2
                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 539 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
234 AlaArgLeuGlnValProProAlaArgThrProSerSerPro...ArgCy 249
                    227 ......CCATCCAGTCCAGCGCACTG 246
                                                                         217 erProAsnAlaAlaValLeuTrpLeuTrpSerSerHisAsnArgValAsn 233
                                                                                                                186 GGATGTCAGCAGGAGTTTGTGGAGGAGTTCATCTGGCCGG..... 226
                                                                                                                                                                                           136 GAAGCCAGGAAGAAGGCACTGAAGCTTGGGGGCCAAAAAGGTGTTCATTGA 185
                                                                                                                                                                                                                                185 ProSerHisProArgLeuAlaAlaLeuLeuLeuArgLeuProArgLeuAr 201
                                                                                                                                                     201 gLysProLeuArgAlaAspAlaAlaAlaSerMetHisArgValGly...S 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/735,041A FILING DATE: 22-0CT-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 805.447.4112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1840 CONTY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                   98 CCTATCTGGCCAACATTGGCC.....AGAAGGAAGGAAGACTTCGAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           592 rargAlaGluGlyAlaProArgSerAlaGluGln 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 539 um.__
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mazza, Richard J. REGISTRATION NUMBER: 27,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91320-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Amgen Inc.
1840 De Havilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         805.499.6751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yabkowitz, Rachel
VENTION: PLACENTAL-DERIVED PROSTRATE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martin, Francis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Farrell, Catherine L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                              127.00
0.760
40.732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                            Length: 410
Gaps: 26
Percent Identity: 25.366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A-414
```

	nuisvaluislenProGlyGlnAspLysAlaLeuAsnArgMetLeuA 48	. v
04	GGCCTAGCCCTGAGTGTGAATTTGTCCG 100	
٢	5 AspIleSerLeuCysValGlyLeuTyrProCysProSerTrpAlaCysTr 47	
6	3CTGAGCTGGTGTATACCGGTTTAC97	95
4	1GlyGlnTrpLeuGlnValLeuGlyGlyGlyPheSerTyrLeu 45	<u>~</u>
2	4 AATCAAACAAGGCCTGGGCTTGAAATTTG	
0	7TrpThrGlyArg.	43
ω	ATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCA	
σ.	SerLeuArgProAlaGlyGlyProSe	
ω	ATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGCAGCCATCCTTTA	
7	::: ::: erGlyAlaTrpAlaAlaAlaProSerTr	ب نس
w	GTGGGCCGTATTGACATCGTGGAGAACCGCTTCI	y or
- '	rgThrAlaSerGlyAlaLeuTrpA 41	75
	GluproLeuGlyGlnTrpHisLeuArgSerGluTnrGlnuTyeuni 39	00
	CAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCA	708
	CCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGGAGATCGAGATCGAGTTCAAAAAAAGGGGTCCCTGGAGATCAGGTTCAGAGATCAGAGAGAG	658 369
	uHisProGlyLeuArgAlaAlaProGlyGlnGluPro	ហ
	ACACGAAGACCCCAGGA	N
	CGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCG 	570 340
	:::	Ñ
	CAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCAGCT	520
	CAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCCATCCCGGT	7
	:::	95
	TCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC	
	ATCAGGICCGGTTTGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	70
	erThrSerSerArgProThrSerProGln.	
	AGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGAAC 36	
		99
	NO TO THE TOTAL OF THE PROPERTY OF THE PROPERT	7 ;
	26	47
	いいのようなできなが	

```
seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-09-190-476B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09190476B
patent No. 6025204
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                  MOLECULE TYPE: US-09-190-476B-2
                                                                                                                                                                                                                        alignment_scores:
                                                                                                               alignment_block:
US-09-775-693-1 x US-09-190-476B-2
                                                                       Align seg 1/1 to: US-09-190-476B-2 from: 1 to: 539
                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1096 CCACTGTCTCTCTACAATGAGGAGCTGG 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1055 CCGTCCTCAAGGGCCAGGTGTACATCC......TCGGCCGGGAGTCC 1095
                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 805.499.6751
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 22-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Farrell, Catherine L.
APPLICANT: Martin, Francis H.
APPLICANT: Yabkowitz, Rachel
TITLE OF INVENTION: PLACENTAL-DERIVED PROSTRATE GROWTH
TITLE OF INVENTION: FACTOR
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    521 oCysSerLeuSerGlyLeuGluValTrp 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             505 IleSerArgHisLeuLysProProAspProIleProSerProProThrPr 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
COPPUTATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 154v CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805.447.4112
98 CCTATCTGGCCAACATTGGCC.....AGAAGGAAGACTTCGAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/190,476B FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: Sir
                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                        Quality:
                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Amgen Inc.
1840 De Havilland Drive
                                                                                                                                                                                                                                                                                                                                                                                539 amino acids
                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                       0.760
40.732
                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                            127.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 08/735,041
                                                                                                                                                                         Percent Identity: 25.366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A-414
```

49 sSerGlyHisProValAsnPheValLeuProAlaThrMetAsnAlaTrp. 70 CACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATGCCCC
20 AGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGAAC
70 GATCAGGTCCGGTTTGAGCTCAGCTGCTACTGACTGGCCCCCCAGATAAA 4
20 GGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGC :::
IGATGGAGTACGCAAAGCAACACGGGATTCCCATCCCGGT ::::::::::::::::::::::::::::::::
328 yLysprodiuMetMetLysSerProThrAsnThrT 340 570 CGAGGCTGGAATCCTGGAGAACCCCAAGAACCAGGCCTCCAGGTCTCT 619 11
AGACCCAGGACCCAGCCAAAGCCCCAACACC 6
TACCTGAACGAAGTCGCGGCAAGCATGGC 786
GGCACCATCCTTTAC 87
74 CATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAA 92: 37TrpThrGlyArg44

HG		PRIOR APPLICATION: PRIOR APPLICATION NUMBER: US 08/735,041 FILING DATE: 22-0CT-1996 ATTORNEY/AGENT INFORMATION: NAME: MAZZA, Richard J. REGISTRATION NUMBER: 27,657 REFERENCE,DOCKET NUMBER: A-414 TELECOMMUNICATION INFORMATION: TELEPHONE: 805,447.4112 TELEPAX: 805,499.6751 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 539 amino acids TYPE: amino acid STRANDEDNESS: single FOPOLOGY: linear MOLECULE TYPE: protein US-09-190-889A-2	RM: py disk pompatible PC-DOS/MS-DOS PRelease #1.0, Version #1. DATA: US/09/190,889A	IMENIATION_block: LOC 2, Application US/09190889A LOC 2, Application US/09190889A LOCANT: Farrell, Catherine L. LICANT: Martin, Francis H. LICANT: Martin, Francis H. LICANT: Yabkowitz, Rachel LE OF INVENTION: PLACENTAL-DERIVED PROSTRATE LE OF INVENTION: FACTOR IBER OF SEQUENCES: 12 BER OF SEQUENCES: 12 CRESTONDENCE ADDRESS: DDRESSEE: Angon Inc. TREET: 1840 De Havilland Drive TY: Thousand oaks	123 30 .pep:US-09-190-889A-	924 AATCAAACAAGGCCTGGGCTTGAAATTTG
----	--	--	--	---	-----------------------------------	-----------------------------------

CGTGGAGAACCGCTTCATTG 823

```
alignment_block:
US-09-775-693-1 x US-09-190-938B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-09-190-938B-2 from: 1 to: 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 127.00 Length: 410
Ratio: 0.760 Gaps: 26
Percent Similarity: 40.732 Percent Identity: 25.366
658 CCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGAC 707
                                                                 620 ACACGAAGACCCAGGA......CCCAGCCAAAGCCCCCAACACC 657
                                                                                                                                                        340 hr.ProHisValProAlaGluGlyProGluAlaSerArgProProLysLe 356
                                                                                                                                                                                                      570 CGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCT 619
                                                                                                                                                                                                                                                  328 yLysProGlu......MetMetLysSerProThrAsnThrT 340
                                                                                                                                                                                                                                                                                                   520 ACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCAGCTA 569
                                                                                                                                                                                                                                                                                                                                              312 AlaMetGlyAlaLeuGluLeuGluSerArgAsnSerThrLeuAspProGl 328
                                                                                                                                                                                                                                                                                                                                                                                          470 GCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCCATCCCGGTC 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                              420 GGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCC 469
                                                                                                                                                                                                                                                                                                                                                                                                                                        295 euGlyGlnLeuProGluGlyCysAlaGluCysAlaAlaAlaProGluLeu 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 .....AlaThrSerSerTrpThrSerLeuGlnL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 GATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 Ser......ThrSerSerArgProThrSerProGln...... 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 AGCGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGAAC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 ......MetCysProCysGlyThrTrpLysProPro 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 CACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCCC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 sSerGlyHisProValAsnPheValLeuProAlaThrMetAsnAlaTrp. 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 TATG......AGGACCGCTACCTCCTGGG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 AlaArgLeuGlnValProProAlaArgThrProSerSerPro...ArgCy 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 .....CCATCCAGTCCAGCGCACTG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 erProAsnAlaAlaValLeuTrpLeuTrpSerSerHisAsnArgValAsn 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 GGATGTCAGCAGGGAGTTTGTGGAGGAGTTCATCTGGCCGG...... 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 gLysProLeuArgAlaAspAlaAlaAlaSerMetHisArgValGly...S 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 GAAGCCAGGAAGAAGGCACTGAAGCTTGGGGGCCAAAAAGGTGTTCATTGA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 ProSerHisProArgLeuAlaAlaLeuLeuLeuArgLeuProArgLeuAr 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 CCTATCTGGCCAACATTGGCC......AGAAGGAAGACTTCGAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 539 amino acids TYPE: amino acid
```

KICA	a
D.C.	STATE: Texas
	CITY: Houston
ırkee	ADDRESSEE: Arnold, White & Dur
	CORRESPONDENCE ADDRESS:
ND COMPOSITIONS FOR THE EXPRESSION OF D PROSTATE DERIVED GROWTH FACTOR	TITLE OF INVENTION: A BONE AN
	APPLICANT: TELEFAX: (512)499
199-4462	APPLICANT: TELEPHONE NO: (512
ates of America	APPLICANT: COUNTRY:
	APPLICANT: STATE:
11011	APPLICANT: STREET: 201 West
THE UNIVERSITY OF TEXAS SY	APPLICANT: NAME: BOARD OF
261	ion_block: Application PC/TUS95092 ORMATION:
S_COMB.pep:PCT-US95-09261-2	<pre>seq_name: /cgn2_6/ptodata/2/iaa/pcTUS_</pre>
p 530	521 oCysSerLeuSerGlyLeuGluValTrp
G 1123	1096 CCACTGTCTCTACAATGAGGAGCTGG
ProlleProSerProProThrPr 521	505 IleSerArgHisLeuLysProProAspPro
TCGGCCGGGAGTCC 1095	1055 CCGTCCTCAAGGGCCAGGTGTACATCC
AGTGGAAGGGAAAGTGCAGGTGT 1054 	488 laThrLeuGlnProGluProProGlyGluGluAlaGlyGluGlyAlaAla
3pLysAlaLeuAsnArgMetLeuA 488	ONE GOISTORIA
······GGCCTAGCCCTGAGTGTGAAT TTGTCCG 1004	471 pHiston
rProCysProSerTrpAlaCysTr 471	oo AspileSer
976	5 3
LeuGlyGlyGlyPheSerTyrLeu 454	41GlyGlnT
TTG952	924 AATCAAACAAGGCCTGGGCTTGAAATTTG
TrpThrGlyArg 440	7
CACCATGGACCGGGAAGTGCGCAA 923	
gProAlaGlyGlyProSer 436	428SerLeuArgProAlaGlyGlyProSer
ACCCCAGCAGGCACCATCCTTTAC 873	824 GAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGCAGCACCATCC
PAlaAlaProSerSerTrpSerThr 427	rgSerGlyAlaTr
. 3	U.S.
GTACCTGAACGAAGTCGCGGGCAAGCATGGC 786	755 TGTACCTGA
gSerGluThrGlnGlyLeuHi 397	luProLeuGlyGln
A 7	708 CAACGTCAAGGATGGCACCACCCA
.ValGlnArgAsnGluGlnAsp 381	369 roGluHisMetAlaAspValGlnA

."

136 GAAGCCAGGAAGAAGGCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGA 185	G 13	OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/09261 FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION: PRIOR APPLICATION: OLASSIFICATION UNMBER: US 08/283,701 APPLICATION NUMBER: US 08/283,701 APPLICATION UNMBER: US 08/283,701 APPLICATION UNMBER: 34,430 REGISTRATION NUMBER: 34,430 REGISTRATION NUMBER: 34,430 REGISTRATION NUMBER: 34,430 REGISTRATION NUMBER: 370 REFERENCE/DOCKET NUMBER: UTFC422P-TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000 TELEPAX: (713) 789-2679 TELEFAX: (713) 789-2679 TELEFAX: 79-0924 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 539 amino acid TOPOLOGY: linear MOLECULE TYPE: protein PCT-US95-09261-2
--	------	--

<pre>seq_documentation_block: ; Sequence 73, Application US/08642255 ; patent No. 5773249 ; GENERAL INFORMATION: APPLICANT: CAPPELLO, Joseph APPLICANT: CAPPELLO, Joseph APPLICANT: HERRARI, Franco A. APPLICANT: HIGH Molecular Weight Collagen-Like ; TITLE OF INVENTION: High Molecular Weight Collagen-Like</pre>	<pre>seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-08-642-255-73</pre>	CTGG 1123	1055 CCGTCCTCAAGGGCCAGGTGTACATCCrcgGcCcGGGAGTCC 109	TGT 10	AGTGTGAATTTGTCCG 100 :::::: ::::: AlaLeuAsnArgMetLeuA 488	AC	pheserTyrLeu 45	4 2	824 GAATGAAGTCCCGAGGTATCTACGAGACCCCCAGCAGCAGCATCCTTAC 8/3	CATTG 82	AGCATGGC 78	CTTCA 75	38	. p - 6	AGGTCTCT 61 ::: ProLysLe 35	⊣—⊅ 3 °	::: :: 12 LeuAspProGl 32	1000
---	---	-----------	---	--------	---	----	-----------------	-----	---	----------	-------------	----------	----	---------	-------------------------------	------------	-----------------------------	------

414 nGlyproAlaGlyProGly.GlySerArgGlyAspProGlyProProGly 430 1162 GCCACCGGG 1170 431 AlaGlngly 433
100 GUCCAGGTGTACATCCTCGGCCGGGGAGTCCCCACTGTCTCTACA 1111
-
865 ATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGA 914
_
409 CCCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCCATCCCGGT 518
AlaGinglyP 23
419 AGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGC 468

-	

```
OM of: US-09-775-693-1 to: PIR_68:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Date: Feb 12, 2002 3:54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database sequences: 219241
Database length: 76174552
Search time (sec): 92.790000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query length: 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query: US-09-775-693-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database: PIR_68:*
                                                                                                                                                                                                                                                                                     pir2:F69034
pir2:E70621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pir1:AJHURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      score_list:
                                                                                                                        pir2:G85980
pir1:JN0506
pir2:G82737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pir1:AJMSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -MODEL-Frame+_12p.model -DEV*XLP
-MODEL-Frame+_12p.model -DEV*XLP
-Q=/Cgn2_1/USPT0_spool/US9977563/runat_12022002_124152_1344/app_query.fasta_1.1315
-Q=/Cgn2_1/USPT0_spool/US9977563/runat_12022002_124152_1344/app_query.fasta_1.1315
-DEPIR_68 -QFMT=-Fastan -SUFEXX-rpr -GAPOD=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOD=4.500
-QGAPEXT=7.000 -XGAPOD=10.000 -XGAPEXT=0.500 -FGAPOD=6.000
-GGAPEXT=7.000 -XGAPOD=10.000 -YGAPEXT=0.500 -DELOP=6.000
-GAPEXT=7.000 -YGAPOD=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START-1 -MATRIX-blosum62 -TRAMS=human40.cd1
-LIST-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0
-LIST-45 -MODE=LOCAL -OOTFMT=pfs -NORM-ext -MINLEN=0
-ALICN=15 -MODE=LOCAL -OOTFMT=pfs -NORM-ext -MINLEN=0
-ALICN=15 -MODE=LOCAL -OOTFMT=pfs -NORM-ext -MINLEN=0
-ALICN=15 -MODE=LOCAL -OOTFMT=pfs -NORM-ext -MINLEN=0
-MAXLEN=200000000 -USER-US09775693_@CGN1_1_76 -NCPU=6 -ICPU=3
                                                                                                                                                                                                                                                                                                                                                                                                                                       pir2:E84935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pir2:T40457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pir1:AJBORS
                                                                                                                                                                                                                                                                                                                       pir1:AJMXRV
                                                                                                                                                                                                                                                                                                                                     pir2:E64353
                                                                                                                                                                                                                                                                                                                                                                                      pir2:S76929
                                                                                                                                                                                                                                                                                                                                                                                                        pir2:D86640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pir2:C83204
                                                                                                                                                                                                                                                                                                                                                                                                                      pir2:B70398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LONGLOG -NO_XLPXY -WAIT -THREADS=1
                                                                                                          pirl:AJSMRC
                                                                                                                                                                                                        pir2:F82025
                                                                                                                                                                                                                                                         pir2:JC4548
                                                                                                                                                                                                                                                                        pir1:AJMZRB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oir2:B69589
                                                                                                                                                                                                                                           :C84394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     815.
807.
                                                                                                                                                                                                                                           670.
539.
                                                                                                                                                                                                                                                                                                           731
692
                                                                                                                                                                                                                             417
                                                                                                                                                                391
                                                                                                                                                                              391
                                                                                                                                                                                                                                                                                                                                                                                                                           . 500
                                                                                                                                                                                                                                                                                            .00
                                                                                                                                                                                                                                                                                                                                                                                           00
                                                                                                                                                                                                                                                                                                                                                                          1000.36
                                                                                                                                                                                                                                                                                                                                                                                                         1065.56
1057.71
1048.52
1017.57
                                                                                                                           982.78

956.87

956.00

906.00

907.44

892.87

892.87

892.87

893.87

877.00

537.90

537.90

535.99

536.88

506.88

599.55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          out_format : pfs
                                                                                                                                                                                                             7.9e-32
7.7e-23
1.3e-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.7e-72
9.4e-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.4e-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4e-144
0.0012
0.0059
0.0090
0.0140
0.0127
                                                                              6.5e-05
0.0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.4e-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EScore Len
                                                                                                                               3.5e-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .5e-145
                                                                                                                                                                                                                                                                            1.5e-43
1.3e-42
2.4e-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1e-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .4e-150
                                                                                                                                                                                                                                                                                                                                                                            .5e-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .6e-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .6e-52
                                                                                                                                                                                                                                                                                                                                                                                                                            .1e-51
                                                                                                                                                                                                                                                                                                                                                                                                                                            .6e-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .7e-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3e-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .5e-68
                                                                                                                                                                                                                                                                                                                           .6e-46
                                                                                                                                                                                                                                                                                                                                                                                                             .7e-49
                                                                                                                                                                .8e-21
                                                                                                                                                                                .8e-21
                                                                                                                                                                                               .6e-22
                                                                                                                                                                                                                                                              .9e-41
                                                                                                                                                                                                                                                                                                                                              4e-47
                                                                                                                                                                                                                                                                                                                                                            4e-47
                                                                                                                 .3e-16
                                                                                                                                                .6e-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ! Documentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         argininosuccinate synthase argininosuccinate synthase argininosuccinate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                  argininosuccinate synthase (EC argininosuccinate synthase (cit argininosuccinate synthase argininosuccinate synthase (EC argininosuccinate synthase (EC argininosuccinate synthase - Ac argininosuccinate synthase - Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           argininosuccinate synthase (EC arginosuccinate synthase - Deir argininosuccinate synthase PASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              argininosuccinate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             argininosuccinate synthase
                                                                                                                                                                                                                                                                                                         argininosuccinate synthase (EC argininosuccinate synthase (EC argininosuccinate synthase - Me
                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Synechoc
argininosuccinate synthase VC26
argininosuccinate synthetase (a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             argininosuccinate synthase
                                                                                                                                                                                                                                                            probable argG protein - Mycobac
argininosuccinate synthase (EC
argininosuccinate synthase (EC
                                                                                                                                                                                                                                                                                                                                                                                                           argininosuccinate synthase (EC
                                                                                                                                                                                                                                argininosuccinate synthase
                                                                                                                                                                                                                                                argininosuccinate synthetase
                 salivary proline-rich glycoprot
BHLF1 protein - human herpesvii
                                                                                                                                                                                                 argininosuccinate synthase
                                                                                                                                                                                                                 argininosuccinate synthase
                                                                                                                   argininosuccinate
                                                                                                                                  argininosuccinate synthase
                                                                                                                                                  argininosuccinate synthase
                                                                                                                                                                  argininosuccinate synthetase
                                                                                                                                                                                argininosuccinate synthase
   hypothetical protein
                                               En/Spm-like transposon protein unconventional myosin-15 - hum
                                                                                probable mucin DKFZp434C196.1
                                                                                       hypothetical 119.5K protein (vorce)
          - Deinocod
                                                                                                                                                                                      pir1:EEWTHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pir2:S50832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: pir1:AJHURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A01195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: I56310
                                                                                                                                                                                                                                                         alignment_block:
US-09-775-693-1 x AJHURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics
                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                        percent Similarity:
                                                                                                                                                                                                                        Align seg 1/1 to: AJHURS
                                                         101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG
                                                                                                                        51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                          34 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys
                                                                                            17
                                                                                                                                                       rSerCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT
                                         Quality: 2144.00
                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                           5.204
100.000
```

from: 1 to: 412

150 34

50

Gaps: 0
Percent Identity: 100.000

```
C;Species: Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 18-Jun-1999
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 18-Jun-1999
C;Accession: A01195; $06104; 156310
C;Accession: A01195; $06104; 156310
R;Beck, H.G.O.; Su, T.S.; O'Brien, W.E.; Beaudet, A.L.
R;Beck, H.G.O.; Su, T.S.; O'Brien, W.E.; Beaudet, A.L.
R;Beck, C. Su, T.S.; O'Brien, W.E.; Beaudet, A.L.
R;Beaudet, A.L.
R;Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pir1:CGHU1B
pir2:E29149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:x01630; NID:g28871; PIDN:CAA25771.1; PID:g28872
R;Isashiki, Y.; Noda, T.; Kobayashi, K.; Sase, M.; Saheki, T.; Titani, K.
Protein Seq. Data Anal. 2, 283-287, 1989
A;Title: Identification of essential arginine residue(s) for Mg-ATP binding of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            argininosuccinate synthase (EC 6.3.4.5) - human
N;Alternate names: citrulline--aspartate ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 148-161 <ISA>
A;Residues: 148-161 <ISA>
R;Residues: 148-161 <ISA>
R; Ainno, Y; Nomiyama, H; Matuo, S.; Shimada, K.; Matsuda, I.; Saheki, T.
R; Jinherit. Metab. Dis. 8, 157-159, 1985
A;Title: Structure of the 5' end region of the human argininosuccinate synthetase gen
A;Reference number: 156310; MUID:87113889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S06104; MUID: 89367258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-24 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:ASS
A;Cross-references: GDB:119010; OMIM:215700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M34903; NID:g179045; PIDN:AAA51782.1; PID:g179047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: translated from GB/EMBL/DDBJ
C;Superfamily: argininosuccinate synthase
C;Superfamily: arginine biosynthesis; ATP; homotetramer; ligase; urea cycle
C;Keywords: arginine biosynthesis; ATP; homotetramer; ligase; urea cycle
F;148-161/Region: ATP binding #status experimental
F;149,153/Binding site: Mg-ATP (Glu, Arg) #status predicted
                                                                                                                                                                                                                                                            A; Description: catalyzes the formation of argininosuccinate from citrulline and
                                                                                                                                                                                                                        A; pathway: urea cycle
                                                                                                                                                                                                                                                                                                                                                                                 defects in this gene may cause citrullinemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                       9q34.1-9q34.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141.50
139.50
139.00
138.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164.59
178.72
164.75
167.45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.0209
0.0192
0.0293
0.0293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | collagen alpha 4(IV) chain
| proline-rich protein - mouse
| atrophin-1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! glutenin, high molecular wei
                                                                                                                                                                                                                                                                                                                                        aspar
```

```
1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCCACT 1100
                                                                       1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                                    334 alargHisCysIleAlaLysSerGlnGluArgValGluGlyLysValGln 350
                                                                                                         317 eAlaGluLeuValTyrThrGlyLeuArgProSerProGluCysGluPheV 334
                                                                                                                            951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                301 ThrMetAspArgGluValArgLysIleLysGlnGlyLeuGlyLeuLysPh 317
                                                                                                                                                                                                                     901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGGCTTGAAATT 950
                                                                                                                                                                                                                                                       801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 PheMetTyrLeuAsnGluValAlaGlyLysHisGlyValGlyArgIleAs 267
                                                                                                                                                                                                                                                                                                                                                                                                                                      751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 oAsnThrProAspIleLeuGluIleGluPheLysLysGlyValProValL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCCAGGACCCAGCCAAAGCCCC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 snLeuMetHisileSerTyrGluAlaGlyileLeuGluAsnProLysAsn 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 CGGGATTCCCCATCCCGGTCACTCCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 erLeuAlaProGlnIleLysValIleAlaProTrpArgMetProGluPhe 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 yAlaThrGlyLysGlyAsnAspGlnValArgPheGluLeuSerCysTyrS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 CGCCACAGGAAAGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 LysGinValGluileAlaGlnArgGluGlyAlaLysTyrValSerHisGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCCAAGTATGTGTCCCCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 uPhevalGluGluPheIleTrpProAlaIleGlnSerSerAlaLeuTyrG 84
                                                                                                                                                                                                                                                                                          CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                            sGlyIleProIleProValThrProLysAsnProTrpSerMetAspGluA 184
```

```
C:Superfamily: argininosuccinate synthase C:Keywords: arginine biosynthesis; homotetramer; ligase; urea cycle F:149,153/Binding site: Mg-ATP (Glu, Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X12459; NID:955766; PIDN:CAA30999.1; PID:955767
C;Comment: This enzyme catalyzes the formation of argininosuccinate from citrulline a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AJRTRS from: 1 to: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-412 <SUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S01440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Nucleotide sequence of the cDNA encoding the rat argininosuccinate synthetas A;Reference number: S01440; MUID:89016648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Surh, L.C.; Morris, S.M.; O'Brien, W.E.; Beaudet, A.L. Nucleic Acids Res. 16, 9352, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1999
C:Accession: S01440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         argininosuccinate synthase (EC 6.3.4.5) - rat
N;Alternate names: citrulline--aspartate ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-775-693-1 x AJRTRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: pir1:AJRTRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity: 99.029
                                                                                 251 AGGACCGCTACCTGCGTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCCC 300
                   301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCCACGG
                                                                                                                                                                    151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                             84 luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg
                                                                                                                                                                                                                                                                                                                                                      101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                            67 uPheValGluGluPheIleTrpProAlaValGlnSerSerAlaLeuTyrG 84
                                                                                                                                                                                                                           51 AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspValSerLysGl 67
                                                                                                                                                                                                                                                                                                               34 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys
                                                                                                                                                                                                                                                                                                                                                                                              17 rSerCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetSerSerLysGlySerValValLeuAlaTyrSerGlyGlyLeuAspTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 GluTyrHisArgLeuGlnSerLysValThrAlaLys 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 2086.00
Ratio: 5.113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 96.845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                        350
                                                                                                                                                                                                                                                                                                                   50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367
```

seq_name: pir1:AJMSRS

```
351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 LysGlnValGluIleAlaGlnArgGluGlyAlaLysTyrValSerHisGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                 1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
                                                                                                               1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                          1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                     1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                               851 CCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 alargHisCysIleAspLysSerGlnGluArgValGluGlyLysValGln 350
                                                                                                                                                                                                                                                                                                                                                                                                                            951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 hrProAlaGlyThrIleLeuTyrHisAlaHisLeuAspIleGluAlaPhe 300
  401
                                                                            384
                                                                                                                                                                                                                                 351 ValSerValPheLysGlyGlnValTyrIleLeuGlyArgGluSerProLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGCGCCTCCAGGTCTCTACACGAAGACCCCAGGACCCAGCCAAAGCCCC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrAsnArgPheLysGlyArgAsnAspLeuMetGluTyrAlaLysGlnHi 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sGlyIleProIleProValThrProLysSerProTrpSerMetAspGluA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oAsnThrProAspValLeuGluIleGluPheLysLysGlyValProValL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 334
                                                                      GluTyrHisArgLeuGlnSerLysValThrAlaLys 412
                                       GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                       367
```

```
argininosuccinate synthase (EC 6.3.4.5) - mouse N;Alternate names: citrulline--aspartate ligase C.Species: Mus musculus (house mouse) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1999 C;Date: 30-Jun-1994 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1999 C;Accession: JU0463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-412 <SUR>
A;Residues: 1-412 <SUR>
A;Cross-references: GB:M31690; NID:g192068; PIDN:AAA37266.1; PID:g309111
C;Comment: This enzyme catalyzes the formation of argininosuccinate from citrulline a
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Surh, L.C.; Beaudet, A.L.; O'Brien, W.E. Gene 99, 181-189, 1991
A;Title: Molecular characterization of the murine argininosuccinate synthetase locus.
A;Reference number: JU0463; MUID:91216457
A;Accession: JU0463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: argininosuccinate synthase
C;Keywords: arginine biosynthesis; homotetramer; ligase; urea cycle
F;149,153/Binding site: Mg-ATP (Glu, Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-775-693-1 x AJMSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 35/3; 58/3; 121/3; 142/3; 495/3; 189/2; 199/3; 230/1; 258/2; 280/1; 324/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AJMSRS from: 1 to: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity: 98.786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCCAGGAAGAAG 150
                                             301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                 117 yAlaThrGlyLysGlyAsnAspGlnValArgPheGluLeuThrCysTyrS 134
                                                                                                                                                                                                 351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                              101 ArgGlnValGluIleAlaGlnArgGluGlyAlaLysTyrValSerHisGl 117
                                                                                                                                                                                                                                                                                                                                                                                                   251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 rSerCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 2073.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oaps: 0
Percent Identity: 96.117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
```

```
argininosuccinate synthase (EC 6.3.4.5) - bovine N.Alternate names: citrulline--aspartate ligase C.Species: Bos primigenius taurus (cattle) C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Feb-1997 C:Accession: A33986
R;Dennis, J.A.; Healy, P.J.; Beaudet, A.L.; O'Brien, W.E. Proc. Natl. Acad. Sci. U.S.A. 86, 7947-7951, 1989
                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                             seq_name: pir1:AJBORS
                                                                                                                                                                                                                                                                                                                                                                                                       1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1101
                                                                                                                                                                                                                                                                                                                1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1051 GTGTCCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                401 GluTyrHisArgLeuGlnSerLysValThrAlaLys 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 ValSerValPheLysGlyGlnValTyrIleLeuGlyArgGluSerProLe 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   851 CCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 ysValThrAsnIleLysAspGlyThrThrArgThrThrSerLeuGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             701 AGGTGACCAACGTCAAGGATGCCACCACCACCAGACCTCCTTGGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 oAsnSerProAspValLeuGluIleGluPheLysLysGlyValProValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 GlnAlaProProGlyLeuTyrThrLysThrGlnAspProAlaLysAlaPr 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167
                                                                                                                                                                                                                                                                                                                                                            luProIleAspAlaThrGlyPheIleAsnIleAsnSerLeuArgLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt alargHisCysIleGlnLysSerGlnGluArgValGluGlyLysValGln}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCTGAGCTGGTGTATACCGGTTTACCGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thr {\tt MetAspArgGluValArgLysIleLysGlnGlyLeuGlyLeuLysph}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt hrProAlaGlyThrIleLeuTyrHisAlaHisLeuAspIleGluAlaPhe}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pIleValGluAsnArgPheIleGlyMetLysSerArgGlyIleTyrGluT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sGlyIleProIleProValThrProLysSerProTrpSerMetAspGluA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGGATTCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234
```

```
A;Cross-references: GB:M26198
C;Comment: This enzyme catalyzes the formation of argininosuccinate from citrulline a
C;Superfamily: argininosuccinate synthase
C;Keywords: arginine biosynthesis; homotetramer; ligase; urea cycle
F;149,153/Binding site: Mg-ATP (Glu, Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Title: Molecular definition of bovine argininosuccinate synthase deficiency. A;Reference number: A33986; MUID:90046714
A;Accession: A33986
A;Molecule type: mRNA
A;Residues: 1-412 <DEN>
A;Residues: 1-412 <DEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AJBORS from: 1 to: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-775-693-1 x AJBORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio: 5.039 Percent Similarity: 99.272
                                               601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC 650
                                                                                           184 snLeuMetHisIleSerTyrGluAlaGlyIleLeuGluAsnProLysAsn 200
167
                                                                                                                                                                                                                                             501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                               151 TyrAsnArgPheGlnGlyArgAsnAspLeuMetGluTyrAlaAsnGluHi
                                                                                                                                                                                                                                                                                                                                              451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                           134 erLeuAlaProGlnIleLysValIleAlaProTrpArgMetProGluphe 150
                                                                                                                                                                                                                                                                                                                                                                                                                       401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGGCCAAGTATGTGTCCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 AGGACCGCTACCTCCTGGGCACCTCTCTTGGCAGGCCCTGCATCGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 uPheValGluGluPheIleTrpProAlaIleGlnSerSerAlaLeuTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspIleSerLysGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetSerGlyLysGlySerValValLeuAlaTyrSerGlyGlyLeuAspTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC
                                                                                                                        ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC
                                                                                                                                                                                            sGlyIleProValProValThrProLysAsnProTrpSerMetAspGluA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysGlnValGluIleAlaGlnArgGluGlyAlaLysTyrValSerHisGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 2061.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 94.903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                  167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
```

```
argininosuccinate synthase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Species: 11-Jun-1999 #text_change 21-Ju1-2000
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000
C;Accession: H72210
C;Accession: H72210
R,Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: pir2:H72210
                                                                                                                                                                                                              A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sec A;Reference number: A72200; MUID:99287316 A;Accession: H72210
C;Genetics:
A;Gene: TM1780
C;Superfamily: argininosuccinate synthase
                                                                                                        A; Molecule type: DNA
A; Residues: 1-409 <ARN>
A; Cross-references: GB:AE001816; GB:AE000512; NID:g4982359; PIDN:AAD36844.1; PID:g49823
                                                                            A; Experimental source: strain MSB8
                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                             Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 alArgHisCysIleAlaLysSerGlnGluArgValGluGlyLysValGln 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            951 TGCTGAGCTGGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 hrProAlaGlyThrIleLeuTyrHisAlaHisLeuAspIleGluAlaPhe 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 GluTyrHisArgLeuGlnAsnLysValThrAlaLys 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pileValGluAsnArgPheIleGlyMetLysSerArgGlyIleTyrGluT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
```

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: H72210 from: 1 to: 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-775-693-1 x H72210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 ACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 YLYSGlyAsnAspGlnValArgPheGluLeuThrTyrAlaAlaLeuAsnP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 GAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 ACCTCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 eLeuLysTrpLeuCysGluLysGlyPheAspValIleAlaTyrValAlaA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 PheLysGlyArgThrAspLeuIleAsnTyrAlaMetGluLysGlyIlePr 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 snvalGlyGlnLysAspAspPheValAlaIleLysGluLysAlaLeuLys 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 CCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                  560 ACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 olleLysValSerLysLysArgProTyrSerGluAspGluAsnLeuMetH 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             510 CATCCCGGTCACTCCCAAGAACCCGTGGAGGATGGATGAGAACCTCATGC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 rAspTyrIlePheThrAlaLeuLeuGlyAsnAlaMetTyrGluGlyArgT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 ThrGlyAlaSerLysValTyrValGluAspLeuArgArgGluPheValTh 68
                                                                                                                                                                                                                              660 TGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    710 ACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTCATGTAC 759
                                                                                                                                                                               218 uThrLeuLeuGluIleHisPheGluAsnGlyIleProValLysValValA 235
760 CTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGA 809
                                                                                        235 snLeuLysAspGlyThrGluLysThrAspProLeuGluLeuPheGluTyr 251
                                                                                                                                                                                                                                                                          GluAspValPheThrTrpThrValSerProLysAspAlaProAspGluG1 218
                                                                                                                                                                                                                                                                                                                         CCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCC 659
                                                                                                                                                                                                                                                                                                                                                                        isIleSerHisGluAlaGlyLysLeuGluAspProAlaHisIleProAsp 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 1226.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::|||||:::::||||||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.683
82.222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 59.012
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain 972h-; cosmid c428 C; Genetics: A; Gene: SPDB: SPBC428.05c A; Map position: 2 C; Superfamily: argininosuccinate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-410 <LYN>
A:Cross-references: EMBL:AL034382; PIDN:CAA22280.1; GSPDB:GN00067; SPDB:SPBC428.05c
                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K. submitted to the EMBL Data Library, November 1998 A;Reference number: 221931 A;Accession: T40457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            argininosuccinate synthase - fission yeast (Schizosaccharomyces pombe) c;Speciles: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
                                                                                                          Align seg 1/1 to: T40457 from: 1 to: 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: T40457
                                                                                                                                                                  US-09-775-693-1 x T40457
                                                                                                                                                                                                                                            Ratio: 3.384 Percent Similarity: 81.013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: pir2:T40457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1210 CGTCTCCAGAGCAAG 1224
1160 ATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATATCAT 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1110 CAATGAGGAGCTGGTGATGAACGTGGAGGTGATTATGAGCCAACTG 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1060 CTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTA 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 GlnLeuValLysLys 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1010 GCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGGAAAGTGCAGGTGTCCGTC 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 spSerLysGlyPheIleAsnIleHisAlaLeuArgLeuLys...ValHis 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 rAsnProGluLeuSerSerMetAspValGluGlyGlyPheAspAlaThrA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 TyrLysGlyAsnValMetProValAlaArgTyrSerProTyrSerLeuTy 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 laPheArgLysAlaGlnGluAsnValThrGlyLysValThrValSerIle 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 uIleTyrAsnGlyPheTrpPheSerProGluMetGluPheLeuLeuAlaA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             960 GGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACT 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 LysGluValMetHisLeuArgAspMetLeuAlaProLysPheAlaGluLe 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  910 CGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCT 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     860 GCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGAC 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 laThrIleLeuTrpIleAlaHisArgAspLeuGluGlyIleThrMetAsp 301
                                                                                                                                                                                                                                                                       Quality: 1083.00
Ratio: 3.384
                                                                                                                                                                                                                                  Percent Identity: 54.430
                                                                                                                                                                                                                                                                                       Length:
```

```
307 AlaLeuArgAspGlnPheValThrPheAsnLeuAlaLysIleLeuTyrAs 323
                                                        922 AAAATCAAA...CAAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTATAC 968
                                                                                                                    290 rgThrAlaHisMetAspLeuGluGlyLeuThrMetGluArgGluValArg 306
                                                                                                                                                                          872 ACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGC 921
                                                                                                                                                                                                                             273 rGlyLeuLysSerArgGlyCysTyrGluThrProGlyLeuThrIleLeuA 290
                                                                                                                                                                                                                                                           822 TGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGCAGCACCATCCTTT 871
                                                                                                                                                                                                                                                                                                                                                                            772 GCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAACCGCTTCAT 821
                                                                                                                                                                                                                                                                                                                                            257 AlaArgArgAsnGlyValGlyArgIleAspIleValGluAsnArgPheSe 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 ly...ThrPheSerGlyValValSerIlePheTyrGlnLeuAsnAlaIle 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                722 GCACCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTC 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 rIleHisPheGluLysGlyAlaProThrLysLeu...GluCysLysAspG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         672 GATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATG 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 LysLeuThrValAspProLysAspAlaProAspGluValGluLeuSe 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           622 ACGAAGACCCAGGACCCAGCCAAAGGCCCCAACACCCCTGACATTCTCGA 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 luAlaGlyIleLeuGluAspProSerMetThrProProLysAspMetTrp 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      572 AGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCTAC 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 rThrLysLysProTrpSerMetAspGluAsnIleValHisCysSerTyrG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               522 TCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCAGCTACG 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 LysAspLeuLeuGluTyrAlaAlaAlaLysGlyIleProValThrGlnTh 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472 AATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCCATCCCGGTCAC 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 alileAlaProTrpArgLeuProValPhePheGluArgPheAlaGlyArg 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         422 TCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 TCAGGTCCGGTTTGAGCTCAGCTGGTACTCACTGGCCCCCCAGATAAAGG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 LysGluAsnCysIleAlaValSerHisGlyCysThrGlyLysGlyAsnAs 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 CGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGAACGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 CCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCCCCAG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 GCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACCTCCTGGGCA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 AAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGAGTTCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 hrSerLeuAlaArgProIleIleAlaArgArgGlnIleGlnIleAlaGlu 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 AGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGGGCCCAAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 eProAlaAlaGinAlaAsnAlaIleTyrGluAsnValTyrLeuLeuGlyT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 LysValTyrValGluAspLeuArgGluGluPheIleAsnAspThrValIl 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 luGluAspTrpAspAlaAlaArgGluLysAlaLeuLysValGlyAlaLys 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 uIleGluGluGlyTrpGluValIleCysTyrMetAlaAsnValGlyGlnG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 GAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTGGCCAGA 121
```

969 CGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCA 1018

```
argininosuccinate synthase (EC 6.3.4.5) - yeast (Saccharomyces cerevisiae)
N;Alternate names: citrulline--aspartate ligase; protein O1228; protein YOLO58w
C;Species: Saccharomyces cerevisiae
C;Date: 30-Jun-1992 #sequence_revision O8-Mar-1996 #text_change 23-Mar-2001
C;Date: 30-Jun-1992 #sequence_revision O8-Mar-1996 #text_change 23-Mar-2001
C;Accession: S59291; JQO779; S61721; S66750; S41983
C;Accession: S59291; JQO779; S61721; S66750; S41983
R;Mannhaupt, G.; Vetter, I.; Schwarzlose, C.; Mitzel, S.; Feldmann, H.
submitted to the EMBL Data Library, August 1995
A;Description: Analysis of a 26kb region on the left arm of yeast chromosome XV.
A;Reference number: S59285
A;Accession: S59281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-420 CFEL>
A;Residues: 1-420 CFEL>
A;Cross-references: EMBL:x91067; NID:g984177; PIDN:CAA62528.1; PID:g984184
A;Cross-references: EMBL:x91067; NID:g984177; PIDN:CAA62528.1; PID:g984184
R;Van Vliet, F.; Crabeel, M.; Boyen, A.; Tricot, C.; Stalon, V.; Falmagne, P.; Nakamura, Gene 95, 99-104, 1990
A;Title: Sequences of the genes encoding argininosuccinate synthetase in Escherichia col A;Reference number: JQ0778; MUID:91071613
A;Accession: JQ0779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: pir1:AJBYRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-26,'Ar',29-47,'VL',50-60,'GGLS',65-168,'F',170-315,'L',317-420 <VAN>
A;Residues: 1-26,'Ar',29-47,'VL',50-60,'GGLS',65-168,'F',170-315,'L',317-420 <VAN>
A;Residues: 1-26,'Ar',29-47,'VL',50-60,'GGLS',65-168,'F',170-315,'L',317-420 <VAN>
A;Mannhaupt, G.; Vetter, I.; Schwarzlose, C.; Mitzel, S.; Feldmann, H.

Yeast 12, 67-76, 1996
A;Title: Analysis of a 26 kb region on the left arm of yeast chromosome XV.
A;Reference number: S61713; MUID:96381248
A;Accession: S61721
                                                                                                                                                                                                                                                                                                                                             A;Accession: S66750
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-420 (*FEW)
A;Cross-references: EMBL:Z74800; NID:g1419870; PIDN:CAA99067.1; PID:g1419871; GSPDB:GN00
A;Experimental source: strain S288C
A;Experimental source: strain S288C
A;Experimental source: Strain S288C
A;Carbeel, M; Seneca, S.; Devos, K.; Glansdorff, N.
Curr. Genet, 13, 113-124, 1988
A;Title: Arginine repression of the Saccharomyces cerevisiae ARG1 gene.
A;Reference number: S41983; MUID:88223481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X91067; NID:g984177; PIDN:CAA62528.1; PID:g984184
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R;Feldmann, H.; Mannhaupt, G.; Vetter, I.
submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-420 <MAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown; translation not shown
A;Gene: SGD:ARG1; MIPS:YOL058w
A;Cross-references: SGD:S0005419; MIPS:YOL058w
A;Map position: 15L
                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-26,'AT',29-47,'VL',50-57 <CRA>
A;Cross-references: EMBL:X07070; NID:g3371; PIDN:CAA30106.1; PID:g3372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S66743
                                                                                                                                                                                                                                                                                                             A; Accession: S41983
                                                                                                                                             Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1116 GGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATGCCA 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1069 CAGGIGTACATCCTCGGCCGGGAGTCCCCACTGTCI...CTCTACAATGA 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1166 CCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 nGlyGlnPhePheSerProCysThrArgMetLeuLeuAlaAlaAsnAsnV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  390 erGlyPheIleGlnIleGluSerMetArgLeuArg 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 uLysLeuSerSerMetAspGluLeuGlyGlyPheAspProThrTrpThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 AsnValThrValLeuGlyArgLysSerAspThrAlaHisLeuTyrAspGl 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....
```

```
C;Superfamily: argininosuccinate synthase C;Keywords: arginine biosynthesis; homotetramer; ligase F;148,152/Binding site: Mg-ATP (Glu, Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AJBYRS from: 1 to: 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-775-693-1 x AJBYRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 CCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGAAGGCACTG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 AAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 GGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 ysProAspValLysCysIleThrProTrpArgMetProGluPhePheGlu 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 AGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 IleAspValAlaLysGlnGluGlyCysPheAlaValSerHisGlyCysTh 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 GTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTCTCCCACGGCGCCAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                          507 TCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407 CCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAAC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 LysIleGlyAlaCysLysPheValCysValAspCysArgGluAspPheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 laAsnValGlyGlnGluGluAspPheAspAlaAlaLysGluLysAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 CATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGG 106
                                                                                                                                                                                                                                                                  185 laHisIleSerTyrGluAlaGlyIleLeuGluAspProAspThrThrPro 201
                                                                                                                                                                                                                                                                                                                    557 TGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCG 606
                                                                                                                                                                                                                                                                                                                                                                    168 eProValAlaGlnThrLysAlaLysProTrpSerThrAspGluAsnGlnA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 ArgPheAlaGlyArgLysAspLeuLeuAspTyrAlaAlaGlnLysGlyIl 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457 CGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGAT 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 lLysAspIleLeuPheProAlaValGlnValAsnAlaValTyrGluAspV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTG 56
                                                                                                       657 CCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGGTCCCCTGTGAAGGTGA 706
                                                                                                                                                          202 ProLysAspMetTrpLysLeuIleValAspProMetAspAlaProAspGl 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SerLysGlyLysValCysLeuAlaTyrSerGlyGlyLeuAspThrSerVa 18
                                                  218 nProGlnAspLeuThrIleAspPheGluArgGlyLeuProVaiLysLeuT 235
707 CCAACGTCAAGGATGGCACCACCCACCAGACCTCC.....TTG 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rGlyLysGlyAsnAspGlnIleArgPheGluLeuSerPheTyrAlaLeuL 135
                                                                                                                                                                                                             CCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACAC 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 1069.00
Ratio: 3.351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 50.483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arginosuccinate synthase - Deinococcus radiodurans (strain R1)
C:Sepecies: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: D75490
R:White, O:: Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M: Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M:
S:: Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                      C: Superfamily: argininosuccinate synthase
                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain R1 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-402 <WHI>
                                                                                                                                                                                                                                                                         A; Map position: 1
                                                                                                                                                                                                                                                                                                     A;Gene: DR0674
                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE001924; GB:AE000513; NID:g6458372; PIDN:AAF10250.1; PID:g645837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1 A;Reference number: A75250; MUID:20036896
A;Accession: D75490
                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: pir2:D75490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1189 CTCAGGCTGAAGGAATATCATCGTCTCCAGAGCAAGGTCACT 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1139 AGGGTGATTATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCC 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1092 GTCCCCACTG...TCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGC 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1042 AAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGA 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402 IleArgIleLysLysTyrGly.....GluSerLysLysThr 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385 euThrGlyPheLeuProThrAspThrThrGlyPheIleAlaIleGlnAla 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 rThrLysThrGluLysLeuTyrAspProThrGluSerSerMetAspGluL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352 ThrValArgValArgLeuTyrLysGlyAsnValIleIleLeuGlyArgSe 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 ysGluTyrIleArgSerMetIleGlnProSerGlnAsnSerValAsnGly 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           992 GTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGG 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 rProAsnTyrSerArgLeuIleTyrAsnGlyPheLeuLeuHisProGluC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            942 CTTGAAATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGT 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 GlyLeuThrLeuAspLysGluValArgGlnLeuArgAspSerPheValTh 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              895 GCCTTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGC...CTGGG 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 yrGluGlnAlaProLeuThrValLeuArgLysAlaHisValAspLeuGlu 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      845 ACGAGACCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAG 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 gIleAspIleValGluAspArgTyrIleAsnLeuLysSerArgGlyCysT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     795 TATTGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCT 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 AspValPheLeuAlaAlaSerAsnLeuAlaArgAlaAsnGlyValGlyAr 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          745 GAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCG 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 hrTyrThrAspAsnLysThrSerLysGluValSerValThrLysProLeu 251
                                                                                                              Quality: 1034.00
                                                                                        Ratio:
                                                     76.886
                                                                                        3.272
                                            Percent Identity:
                                                                                                           Length:
```

```
US-09-775-693-1 x D75490 ..
Align seg 1/1 to: D75490 from: 1 to: 402
```

854 CAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACC 903 804 CGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCC 853 259 uValGluAsnArgPheValGlyMetLysSerArgGlyValTyrGluThrp 243 ThrLysAlaAsnGluIleAlaGlyArgHisGlyValGlyArgIleAspLe 754 ATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACAT 803 231 leAsnGly......GluGlnLeuSerProAlaAlaLeuLeu 242 704 TGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTC 753 214 rGluAlaGluTyrValGluIleGluTyrValAsnGlyAspProValSerI 231 654 CACCCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGAAGG 703 198 ProProThrHisMetPheLysLeuThrValAsnProGluAspAlaProSe 214 604 GCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAA 653 181 etLeuHisIleSerTyrGluGlyGlyProLeuGluAspProTrpThrGlu 197 554 TCATGCACATCAGCTACGAGGCTGGAGATCCTGGAGAACCCCAAGAACCAA 603 164 yIleProValProThrThrLysLysAspProTrpSerMetAspAlaAsnM 181 504 GATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACC 553 150PheGlnGlyArgAlaAspLeuGluAlaPheAlaArgGluHisGl 164 454 AACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGG 503 135 euLysProAspIleValThrValAlaProTrpArgAspTrpAsp..... 149 404 TGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTAC 453 118 aThrGlyLysGlyAsnAspGlnValArgPheGluMetSerAlaTyrAlaL 135 354 CACAGGAAAGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCAC 403 102 MetValGluTleAlaGluLysGluGlyAlaValAlaIleSerHisGlyAl 118 304 CAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGC 353 254 ACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAA 303 204 TGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGG 253 154 CTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTT 203 104 TGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCA 153 85 lyTyrTyrLeuLeuGlyThrSerIleAlaArgProLeuIleAlaLysLys 101 68 eValArgAspTyrValPheProMetMetArgSerSerAlaLeuTyrGluG 85 52 LeuAsnThrGlyAlaValAlaAlaTyrAlaLeuAspLeuArgGluGluph 68 35 hraiaAspLeuGlyGlnGlyAspGluValGluGluAlaArgValLysAla 51 18 eIleLeuLysTrpLeuGlnThrGluArgAsnTyrAspValValCysPheT 35 57 CATCCTCGTGTGGCTGAAG...GAACAAGGCTATGACGTCATTGCCTATC 103 2 SerLysGluLysIleValLeuAlaTyrSerGlyGlyLeuAspThrSerIl 18 7 AGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTG 56 276

```
argininosuccinate synthase PA3525 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: C83204 R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd A;Reference number: A82950; MUID:20437337
A;Accession: C83204
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: pir2:C83204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-405 <STO>
A; Cross-references: GB:AE004773; GB:AE004091; NID:99949672; PIDN:AAG06913.1; GSPDB:GN00:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain PAO1 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: argG; PA3525
C;Superfamily: argininosuccinate synthase
                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                   alignment_block:
US-09-775-693-1 x C83204
                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                 Align seg 1/1 to: C83204 from: 1 to: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1042 AAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGA 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1192 AGGCTGAAGGAATATCATCGTCTCCAGAGCAAG 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1142 GTGATTATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTC 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1092 GTCCCCACTGTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGG 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  954 TGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAA...... 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               904 ATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGC 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 salaGluArgSerLeuTyrAspLysAspLeuValSerPheGluAlaGlyG 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 ThralaargLeuLysLeuTyrLysGlyAsnCysIleValalaGlyArgLy 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 lnValTyrPheAspHis...ValAlaLysSer......ValThrGly 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        997 ....TTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGG 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 lyAspTyrAsnGlnHisAspAlaGlyAlaPheIleLysLeuAsnSerLeu 388
51 CTCGTGCATCCTCGTGTGGCTGAAGGAA...CAAGGCTATGACGTCATTG 97
                                                                                       ArgMetArgValGlnLysArgValGluAspLys 399
                                                                                                                                                                                                                                                                                                         927.50
3.011
76.238
                                                                                                                                                                                                                                                                                                            Gaps: 6
Percent Identity: 47.030
                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                404
```

104	92	
991 325	42 CTTGAAATTTGCTGAGCTGGTGTATACCGGTTTACC ::: ::: ::: 08 tProLysTyrAlaSerLeuIleTyrThrGlyTyrT)	3 9
	92 GAGGCCT :::: 92 GluSerI	N ®
891 291	CTACGA sTyrGl	N δe
841 275	ATT(::: Leu	79
258	2 TTGGAGCT	74 24
741 241	2 TCCCTGTG	69 23
691 230	2 CAAAGCCC ::: 3 uAsnAlaF	64 21
	2 CCCAAGAA :: 7 ThrTrpTh	59 19
591	2 TGGATGAG 0 etAspAla	4 00
	8 ACACGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCA 5 :	16
97	CAA ::	148
447 150	ACTCACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAA 4 ::: ::: :::	398
397 134	CGGCGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCT 3	148
347 117	CGCAAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCA	98
297 100	ATGAGGACCGCTACCTCCTGGGAACCTCTCTTGCCAGGCCCTGCATCGCC	48 84
47	GGAGTTTGT : uGluPheVa	98 67
97 7	AAGGCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAG 1	4.8 5.1
<u> </u>	ACATTGGCCAGAAGGAAGACTTCGAGGA ::::: ::: spLeuGlyGlnGlyGluGluValGluPr	34

```
alignment_block:
US-09-775-693-1 x C81415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Gene: argG; Cj0665c
C;Superfamily: argininosuccinate synthase
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB75297.1; PID:g696812
A;Experimental source: serotype 02, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-406 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: C81415 from: 1 to: 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: pir2:C81415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                       210 GGAGTTCATCTGGGCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                166 GCCAAAAAG......GTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                   116 GCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGCACTGAAGCTTGGG 165
74 sAspTyrValPheProMetPheArgAlaAsnAlaIleTyrGluGlyGluT 91
                                                                          58 IleLysGluGluAsnIlePheIleLysAspLeuArgAspGluPheValLy 74
                                                                                                                                                        41 lyGinGlyGluGluLeuGluProAlaArgLysLysAlaLeuSerLeuGly 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1142 GTGAT...TATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCC 1188
                                                                                                                                                                                                                                         24 pLeuGlnAspGluTyrAsnCysGluValValThrPheThrAlaAspIleG 41
                                                                                                                                                                                                                                                                               69 GCTGAAG...GAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1189 CTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1092 GTCCCCACTGTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGG 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1042 AAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGA 1091
                                                                                                                                                                                                                                                                                                                                             19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              392 LeuArgMetArg 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 lyGlyAlaTyrAsnGlnAlaAspAlaAlaGlyPheIleLysLeuAsnAla 391
                                                                                                                                                                                                                                                                                                                     8 ValValLeuAlaTyrSerGlyGlyLeuAspThrSerIleIleLeuLysTr 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 sSerAspAspSerLeuPheAspAlaAsnIleAlaThrPheGluGluAspG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 ValValArgLeuLysLeuTyrLysGlyAsnValValValValGlyArgLy 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 rgLeuMetLeuGlnGlnMetIleAspAlaSerGlnValAsnValAsnGly 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              892.00
3.014
74.559
                                                                                                                                                                                                                                                                                                                                                                                                                                                    :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 47.355
                                                                                                                                                                                IIII:::IIIIIIIIIIIIII
```

365 rLeup
:: ::: ::::::
32 laLeuileAsgGluSerGlnILeHisAlaAsnGlyArgValLysLeuGlu 348 57 GTCCTCAAGGGCCAGGTGTAAATCCTCCCAATGCCCAAGGCCAGGTGTAAATCCTCCCCAATGCCCAATGCCCAAGGCCAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAG
TOCCAGGACCACTEGACTERMENT TRANSPORTED TO THE TRANSPORT TO
007 GACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGG
157 CAGGCACCATCCTTTACCL :: :82 lyGlyThrIleLeuLeuLy
165 1
"57 TACCTGAACGAAGTCGCG 49 LysLeuAsnGluLeuGly
07 CCAACGTCAAGGATGGCACCACCC ::::: 37 snglyGluLys
20 u
07 cc
57 TGCACATCAGCTACGAGGCTGC ::
CATCCCGGTCACTC
:50 FTCAAGGGCCGCAATGAC
10 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGO
360 AAAGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGGTACTCACTGGCCC 409
0 H
260 ACCTCC7 91 yrLeuLe

1154 CAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGG 1194

```
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hird Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20263314
A;Accession: C84048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         argininosuccinate synthase (citrulline asparate ligase) argG [imported] - Bacillus halod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-409 <STO>
A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB06906.1; GSPDB:GN00
A;Cross-references: GB:AP001518; GB:BA0000004; NID:g10175792; PIDN:BAB06906.1; GSPDB:GN00
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: pir2:C84048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: argG
C;Superfamily: argininosuccinate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio: 2.912
Percent Similarity: 72.439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: C84048 from: 1 to: 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-775-693-1 x C84048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 AAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 CCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 GGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACC 256
                                                                                                                                                                                                                                   357 AGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGG 406
                                                                                                                                                                                                                                                                                    102 ValGluileAlaGluGlnThrGlyAlaGlnAlaValAlaHisGlyCysTh 118
                                                                                                                                                                                                                                                                                                                                          307 GTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                  257 GCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 LysValGlyAlaIleGluSerTyrThrIleAspAlaLysLysGluPheAl 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 euaspValGlyGluGlyLysaspLeuGluPheValLysGluLysalaLeu 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 lalaileLysTrpLeuSerAspLysGlyTyrAspValIleAlaValGlyL 35
                                                                       135 snproAsnLeuGluValLeuAlaProValArgGluTrpAlaTrp..... 149
                                                                                                                           407 CCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAAC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 aGluGluPheValLeuProAlaLeuGlnAlaHisAlaLeuTyrGluGlnL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTG 56
                                                                                                                                                                                                                                                                                                                                                                                              85 ysTyrProLeuValSerAlaLeuSerArgProLeuIleSerLysLysLeu 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGG 106
                 CGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGAT 506
                                                                                                                                                                               rGlyLysGlyAsnAspGlnValArgPheGluValSerTleGlnAlaLeuA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
865.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 44.878
```

```
163 eProIleProIleAspLeuAspAsnProTyrSerValAspGlnAsnLeuT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   507 TCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 .....SerArgAspGluGluIleGluTyrAlaLysLysAsnAsnIl 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 rpGlyArgSerAsnGluCysGlyIleLeuGluAspProTrpAlaThrPro 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     557 TGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCG 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 proGluGlyAlaTyrGluLeuThrValAlaIleGluAspAlaProAspGl 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      657 CCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGA 706
                                                                                                                                                                                                                                                                                                                                           1057 GTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCT 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                            1007 ACTGCATCGCCAAGTCCCCAGGAGCGAGTGGAAAGTGCAAGTGTCC 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      757 TACCTGAACGAACTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGT 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    707 CCAACGTCAAGGATGGCACCCACCCAGACCTCCTTGGAGCTCTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      807 GGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAG 856
                                                                                                                                             1157 CTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATAT 1206
                                                                                                                                                                                                                                               1107 CTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAA 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      907 GACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGA 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 lyalaMetThrLeuIleLysalaHisLysGluLeuGluAspLeuThrLeu 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        857 CAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258 iGluAsnArgLeuValGlyIleLysSerArgGluValTyrGluCysProG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 uLeuIleTyrGluGlyLeuTrpPheSerProLeuGlnProAlaLeuSerA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 ThrLysCluValAlaHisPheLysProValValGluLysLysIleAlaGl 308
                                               1207 CATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                              342 LeuPheLysCiyHisAlaIleValGluGlyArgLysSerGluTyrSerLe 358
                                                                                                                                                                                                                                                                                                                                                                                          325 laPheLeuLysGluThrGinSerThrValThrGlyValValArgValLys 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             957 GCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCC 1006
                                                                                                                                                                                             358 uTyrAsnGluLysLeuAlaThrTyrThrProAspAspGluPheAspHisA 375
                                                                                                 375 snAlaAlaValGlyPheIleSerLeuTrpGlyLeuProThrLysValTyr 391
392 SerMetValAsnLysGluMetLysGluLys 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCCAGGTCTCTACACGAAGACCCAGGGACCCAGCCAAAGCCCCCCAACAC 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..AsnGlyLysSerTyrProValHis......GluLeuIleLeu 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                756
```

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Becc.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

seq_documentation_block: seq_name: pir2:B69589

argininosuccinate synthase argG - Bacillus subtilis

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Roetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Scort T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, F.; Sekiguchi, A.; Tosato, V.; Uchiyama, A.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A.; Cetatus. 2011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: argininosuccinate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: argG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:299118; GB:299119; GB:AL009126; NID:92635411; PIDN:CAB14923.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA A:Residues: 1-403 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: B69589 from: 1 to: 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-775-693-1 x B69589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
151 .....SerArgGluGluGluIleGluTyrAlaAlaSerAr 162
                                                 451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                     134 erLeuAsnProAspLeuGluValIleAlaProValArgGluTrpGlnTrp 150
                                                                                                                                                          401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                 117 yCysThrGlyLysGlyAsnAspGlnValArgPheGluValSerIleLysS 134
                                                                                                                                                                                                                                                                      351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                       101 LysLeuValGlurleAlaGluLysGluAspAiaGlnAlaIleAlaHisGl 117
                                                                                                                                                                                                                                                                                                                                                                               301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                84 luGlyLysTyrProLeuValSerAlaLeuSerArgProLeuIleAlaLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AlaLeuGluValGlyAlaThrAsnSerTyrValIleAspAlaLysGluGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 ysCysLeuAspValGlyGluGlyLysAspLeuAlaPheValGlnGlnLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||
| 17 rSerValAlaIleLysTrpLeuGlnGluGlnGlyTyrAsnValIleAlaC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uPheAlaGlnAspTyrAlaLeuIleSerLeuGlnAlaHisThrMetTyrG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                818.00
2.773
73.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 42.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
```

```
seq_documentation_block:
                                                                                                                               1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                  1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                        1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCCACT 1100
                                                                             374 SpHisHisAlaAlaIleGlyPheIleGluLeuTrpGlyLeuProThrLys 390
                                                                                                                                                                                                                                                                                                                                                                                                                                            1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAAGGGGAAAGTGCAG 1050
                                                                                                                                                                                357 rSerLeuTyrAspGluLysLeuAlaThrTyrThrLysAspAspAlaPheA 374
                                                                                                                                                                                                                                                                                       341 ValLysLeuPhcLysGlyHisAlaIleValGluGlyArgLysSerGluTy 357
                                                                                                                                                                                                                                                                                                                                                                                          324 euHisAlaPheLeuLysGluThrGlnLysHisValThrGlyIleValArg 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 tSerGluIleIleTyrAsnGlyLeuTrpPheSerProLeuLysAspAlaL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 ThrLeuValLysGluValAlaHisPheLysProIleIleGluGlnLysMe 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 ysProGlyAlaMetThrLeuIleLysAlaHisLysGluLeuGluAspLeu 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         851 CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 IleLeuLysLeuAsnGluMetAlaGlyAlaHisGlyValGlyArgIleAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 errle......AspGlyValSerTyrSerLeuSer...GluLeu 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    701 AGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 oAspThrProGluValIleGluIleAlaPheGluGlnGlyValProValS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 AlaProProGluGlyAlaTyrAspLeuThrAlaProLeuGluLysThrPr 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAAGCCCAAAGCCCC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 gGlyTleProTleProTleAsnLeuAspSerProTyrSerTleAspGlnA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHisValGluAsnArgLeuValGlyIleLysSerArgGluValTyrGluC 274
```

seq_name: pir2:T06667

```
A; Experimental source: cultivar Columbia; BAC clone F617
                       A;Cross-references: EMBL:AL049657; GSPDB:GN00062; ATSD:F617.40
                                                                            A; Molecule type: DNA
A; Residues: 1-498 <BEV>
                                                                                                                                        A; Reference number: Z15792
A; Accession: T06667
                                                                                                                                                                      R:Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; submitted to the Protein Sequence Database, April 1999
                                                                                                                                                                                                                                                                         argininosuccinate synthase (EC 6.3.4.5) - Arabidopsis thaliana
N;Alternate names: protein F617.40
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Oct-1999
C;Accession: T06667
```

```
A:Map position: 4
A:Introns: 25/1; 100/1; 146/2; 162/3; 223/3; 285/3; 315/2
C:Superfamily: argininosuccinate synthase
C:Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: ATSP: F617.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-775-693-1 x T06667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: T06667 from: 1 to: 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 GCCAGAAG...GAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 GlyAlaSerGlnLeuValValLysAspLeuThrGluGluPheValLysAs 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 lyGlnGlyIleLysGluLeuGluGlyLeuGluGlnLysAlaLysAlaSer 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 TCCTGGGCACCTCTTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 pPheIlePheProCysLeuArgAlaGlyAlaIleTyrGluArgLysTyrL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 ATCGCCCAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413 AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 ...... 223
                                                                                                                                                                                                                                                                                                                                                                                                                                    236 luLeuLysValValAlaProTrpArgGluTrpGlu......Ile 248
                                                                                                                                                                                                                                                                                                                                                                                        463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGGATTCCCAT 512
                                                                                                                                                                                                                                                                                                                                               249 GlnGlyArgGluAspAlaIleGluTyrAlaLysLysHisAsnValProVa 265
                                                                                                                            613 GGTCTCTACACGAAGACCCAGGACCCAGCCCAAAGCCCCCAACACCCCCTGA 662
                                                                                                                                                                      ::|||:::|||::: :::||||||:::||| ||||:::
282 euSerHisGluGlyAspLeuLeuGluAspProAlaAsnGluProLysLys 298
                                                                                                                                                                                                                  563 TCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                                                            265 lprovalThrLysLysSerIleTyrSerArgAspArgAsnLeuTrpHisL 282
                                                                                                                                                                                                                                                                                                   513 CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                           663 CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                                                   299 AspMetTyrMetMetSerValAspProGluAspAlaProAspGlnProGl 315
315 uTyrIleGluIleGlyIleGluSerGlyLeuProValAlaLeuAsnGly. 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....ValArgPheGluLeuThrPhePheSerLeuAsnProG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        815.00
2.890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 42.172
```

```
seq_name: pir2:E84935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  argininosuccinate synthase (BC 6.3.4.5) [imported] - Buchnera sp. (strain APS)
                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H. Nature 407, 81-86, 2000
                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A84930; MUID:20445173
A; Accession: E84935
                                                                                                                                                                                                                           C; Superfamily: argininosuccinate synthase
                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AP000398; GSPDB:GN00144
                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-403 <STO>
                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                  A, Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp
                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                             C; Keywords: ligase
                                                                                                                                                                                                                                             A; Gene: argG; BU050
                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                  A; Experimental source:
                                        alignment_block:
US-09-775-693-1 x E84935
Align seg 1/1 to: E84935 from: 1 to: 403
                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 .....LysalaLeuSerProAlaThrLeuLeuAlaGluLeu 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       713 TCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATGTACCTG 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            763 AACGAAGTCGCGGGCAAGCATGGCCTGGGCCGTATTGACATCGTGGAGAA 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 AsnThrIleGlyGlyLysHisGlyIleGlyArgIleAspMetValGluAs 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1113 TGAGGAGCTGGTGACCATGAACGTGCAGGGTGATTATGAGCCAACTGATG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1063 AAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 GluSerTleGlnValLysAspThrLeuAlaLeuLysTyrAlaGluMetVa 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  913 GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        377 hrIleLeuPheAlaAlaValGlnGluLeuGluSerLeuThrLeuAspArg 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1163 CCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 lTyralaGlyargTrpPheaspProLeuArgGluSerMetAspAlaPheM 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         963 GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427 etGluLysIleThrGluThrThrThrGlySerValThrLeuLysLeuTyr 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477 lahlaGlyPheIleArgLeuTyrGlyLeuProMetLys 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460 gGlnAspIleSerSerPheGluGlySerGluIleTyrAsnGlnAlaAspA 477
                                                                                                                                        Quality:
                                                                                                                     Ratio:
                                                                                                     807.50
2.710
75.253
                                                                                                                                                                                                                                                                                              strain APS
                                                                                                       Percent Identity: 43.687
```

```
283 hrileileMetThrAlaileLysAlaileGluGlnLeuValLeuAspArg 299
                                        863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG 912
                                                                                                    813 CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCA 862
                                                                              266 nArgLeuileGlyMetLysSerArgGlyCysTyrGluThrProGlyGlyT 283
                                                                                                                                                                 250 AsnSerLeuGlyAlaLysHisGlyIleGlyArgIleAspIleIleGluAs 266
                                                                                                                                                                                                         763 AACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAA 812
                                                                                                                                                                                                                                                 238 lnLys.....LeuAsnProLeuLysCysValGluGluLeu 249
                                                                                                                                                                                                                                                                                         713 TCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATGTACCTG 762
                                                                                                                                                                                                                                                                                                                                    221 uTyrValSerLeuGlnLeuLysGluGlyCysValValSerValAsnAsnG 238
                                                                                                                                                                                                                                                                                                                                                                        663 CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                                                                                                                                                                                                                                                                                                                                                                                     205 ASPCYSTrpSerTrpThrValAsnProGluAspAlaProGluLysProGl 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                             613 GGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCCAACACCCCCTGA 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 leSerThrGluGlyClyLeuLeuGluAsnProTrpAsnGlnSerAsnGlu 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           563 TCAGCTACGAGGCTGGAATCCTGGAGAACCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 rThrAlaThrLeuGluLysIleTyrSerLysAspGluAsnSerTrpHisI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513 CCCGGTCACTCCCAAGAACCCCGTGGAGGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 AsnSerArgGluSerLeuLeuLysTyrLeuAspLysLysAsnIleSerTh 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGGATTCCCCAT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 snLeuAsnVallleAlaProTrpArg.....GluTrp.....AsnLeu 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 LeuAlaLeuAsnIleGlyAlaAsnSerLeuCysHisGlyAlaThrGlyLy 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 ATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 TCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGGCCGGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 euleuGlyThrAlaMetAlaArgProIleIleAlaLysLysGlnValGlu 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 nTyrValTyrProValLeuLysThrGlyAlaLeuTyrGluGlySerTyrL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 GCCAG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 GlyAlaSerSerCysHisValPheAspLeuLysGluGluPheIleGluAs 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 lyGlnSerLysLysAspLeuAsnGlyIleGluLysLysSerLeuGluSer 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 pLeuLysGluAsnTyrAsnPheGluValValAlaPheValAlaAspIleG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCCAACATTG 115
```

```
alignment_block:
US-09-775-693-1 x B70398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: argG
C;Superfamily: argininosuccinate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE000725; NID:g2983598; PIDN:AAC07170.1; PID:g2983600; GB:AE00A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-401 <AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: B70398 from: 1 to: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666
A;Accession: B70398
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity: 72.277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 argininosuccinate synthase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 16-Jul-1999
C;Accession: B70398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: pir2:B70398
                                          160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                        110 ACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGACGCACTGAAG 159
53 AlaGlyAlaIleGluAlaIleValGluAspLeuLysGluThrPheAlaGl 69
                                                                                  36 spValGlyGlnGlyGluGluLeuSerGluIleProGluLysAlaArgArg 52
                                                                                                                                                                1163 CCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1113 TGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383 laAspGlyPheIleArgLeuPheSerLeuSerSerLys 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1063 AAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 rGluGluTyrAlaThrPheGlyGluAspLysValTyrLysGlnSerAspA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 LysGlySerValThrAlaValGlnLysLysSerProAsnSerLeuTyrSe 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 laAspSerLeuSerLeuGluIleThrGlyGluValIleLeuLysLeuTyr 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 lTyrAspGlyArgTrpPheSerProIleArgLysSerLeuGlnAlaAlaA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                963 GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 GluSerPheArgTrpArgGluLysIleGlyLeuGluMetSerSerIleVa 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                913 GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             800.50
2.741
                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 41.832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
```

```
103 TyrTyraladluLysPheAsnAlaAspTyrValAlaHisGlySerThrGl 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 GAAATCGCCCAGGGGAGGGGGCCAAGTATGTGTCCCCACGGCGCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 ACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             510 CATCCCGGTCACTCCCAAGAACCCGTGGAGGATGAGAACCTCATGC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |::: :::||| ::::::|||:::|||:::||||:::|||| 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::||| ||||:::||| |||||:::||| :::::: |||
182 lyValSerIleGluCysGlyProLeuGluAspProTrpGlnGluProPro 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      560 ACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 610 CCAGGTCTCTACACGAAGACCCAGGACCCAAGCCAAAGCCCCGCAACACCCC 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        660 TGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAAGGTGACCA 709
                                                                                                                                                                                                                                                                                                                                                      231 ......AsnGlyGluArgTyrGluGluGlnTrpLysLeuIleAlaAsn 244
                                                                                                                                                                                                                                                                                                                                                                                                                                         710 ACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATGTAC 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 oGluTyrValThrValGlyPheGluLysGlyLysProValTyrLeu.... 230
                                                                                                                                                                                                                                                                                                 810 GAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAG 859
                                                                                                                                                                                                                                                                        860 GCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGAC 909
                                                                                                         1007 ACTECATCECCAAGTCCCAGGAGCGAGTGGAAAGGGAAAGTGCAGGTGTCC 1056
                                                                                                                                                                                                                   910 CGG...GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTTGCTGA 956
                                                                                                                                                                                                                                            278 lametValLeuTyrGluAlaTyrArgAspLeuLeuSerLeuValLeuAsp 294
                                                    1057 GTCCTCAAGGGCCAGGTGTACATCCTCGGCGGGGAGTGCCCACTGTCTCT 1106
                                                                                                                                                                                         295 ArgPheThrPheHisTyrPheLeuThrHisIleProHisGluTyrAlaLy 311
                                                                                                                                                              957 GCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCC 1006
1107 CTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAA 1156
                                                                                ||| ||| ::: ||||::::||| 344
328 laPheThrAsnLySIleAlaGluPheAlaThrGlyGluValArgLeuLys
                                                                                                                                    311 sLeuValTyrCluGlyLeuTrpPheThrProLeuArgGluAlaLeuAspA 328
```

```
Swissprot_39:ASSY_MOUSE + 2073.00 22
Swissprot_39:ASSY_DOVIN + 2069.00 22
Swissprot_39:ASSY_DOVIN = 1164.00 12
Swissprot_39:ASSY_SCHPO + 1083.00 11
Swissprot_39:ASSY_PASSY + 1069.00 11
Swissprot_39:ASSY_BACSU + 818.00 8
Swissprot_39:ASSY_BUCAI + 807.50 8
Swissprot_39:ASSY_BUCAI + 777.00 8
Swissprot_39:ASSY_ACIA + 777.00 8
Swissprot_39:ASSY_SYNY3 + 764.00 8
Swissprot_39:ASSY_ARTIA + 747.00 8
Swissprot_39:ASSY_ARTIA + 747.00 8
Swissprot_39:ASSY_METJA + 747.00 8
Swissprot_39:ASSY_METJA + 747.00 8
Swissprot_39:ASSY_METJA + 764.00 8
Swissprot_39:ASSY_METJA + 682.50 7
Swissprot_39:ASSY_METJA + 682.50 7
Swissprot_39:ASSY_METGL + 670.50 7
Swissprot_39:ASSY_STRCL + 670.50 7
Swissprot_39:ASSY_THEAC + 670.50 7
Swissprot_39:ASSY_THEAC + 670.50 6
Swissprot_39:ASSY_PASMU + 421.00 4
Swissprot_39:ASSY_PASMU + 421.00 4
Swissprot_39:ASSY_PASMU + 421.00 4
Swissprot_39:ASSY_METHH 692.

Swissprot_39:ASSY_METHH 686.

Swissprot_39:ASSY_METHA 686.

Swissprot_39:ASSY_STRCL 670.

Swissprot_39:ASSY_CORGL 630.

Swissprot_39:ASSY_PASMU 421.

Swissprot_39:ASSY_PASMU 421.

Swissprot_39:ASSY_ECOLI 431.

Swissprot_39:ASSY_ETLA 386.

Swissprot_39:ASSY_STRCO 433.

Swissprot_39:ASSY_STRCO 434.

Swissprot_39:ASSY_STRCO 434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Date: Feb 12, 2002 4:11 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database sequences: 100059
Database length: 36664827
Search time (sec): 71.550000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search information block:
Query: US-09-775-693-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SwissProt_39:ASSY_RAT +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query length: 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -MODEL-frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09775693/runat_12022002_124154_1491/app_query.fasta_1.1315
-DB=-SwissBrot_39 -QEMT=fastan -SUFFIX=rsp -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -DELOP-6.000 -DELEXT=7.000 -START=1 -MATRIX-blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM-ext -MINLEN=0 -MAXLEN=2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USER=US09775693_@CGN1_1_36 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of: US-09-775-693-1 to: SwissProt_39:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SwissProt_39:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AN + 214
+ 2086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Orig
                                                                                                                                                                     + 141.5
139.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rig zscore
2144.00 2323.
                                                                                                                                                                                                                                 150.00
144.00
          139.00
138.50
136.00
136.00
136.50
134.50
134.50
                                                                                                                                                                                                                                                                                           391.00
386.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.00 2323.43
.00 2260.62
                                                                                                                                                                                                                50
                                                                                                                                                                                          . 50
                                                                                                                                                                                                                                                                        7 242.5 54

7 242.5 54

7 242.5 51

1174.5 11

986.8 80

986.8 76

987.6 90

887.6 90

887.6 90

881.3 39

881.3 39

881.3 39

881.3 39

881.3 39

881.3 39

881.3 39

881.3 39

881.3 39

881.3 39

881.3 39

881.3 39

881.3 39

881.3 39

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30

881.3 30
                                                                                                                                                                         144.09
                                                                                                                                                                                                                152.14
                                                                                                         143.53
145.84
153.62
                                                                                                                                                                                                                                   160.93
                                                                                            150.77
                                                                                                                                                                                             . 32
                                                                    32 0.1543
0.1997
53 0.2141
34 0.2252
52 0.2972
77 0.3029
56 0.3372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.4e-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EScore Len ! Documentation 3 2.3e-122 412 ! P00966 hg
                                                                                                                                                                                                                0.1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.5e-118
7.8e-118
3.0e-63
                                                                                                                                                                                                                                                                                                                 4.3e-38
3.9e-37
8.3e-34
2.0e-34
1.8e-33
4.6e-31
6.0e-30
2.0e-18
6.0e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.6e-40
4.0e-39
          0.3870
0.4244
0.5160
                                                                                                                                                                                                                                        0.0987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.3e-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.6e-38
                                                                                                                                                                                                                                                         0.0493
                                                                                                                                                                                                                                                                          4.1e-13
                                                                                                                                                                                                                                                                                               2.6e-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.2e-42
3.6e-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..6e-57
5.2e-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5e-41
                                                                                                                                                                         1690
1183 !
                                                                                                                                                                                                                                   1185
838
234
331
660
648
3511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O95zz3 arabidopsis thallana
O34347 bacillus subtilis ar
P57158 buchnera aphidicola
O67213 aquifex aeolicus arg
P57799 lactococcus lactis (s
P77973 synechocystis sp. (st)
O28032 archaeoglobus fulgidu
O60174 methanococcus jannasc
P13256 methanococcus vanniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P09034 rattus norvegicus (rat
                                                                                                                                                                                                                P03181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! P00966 homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                       027322 methanobacteri
p94993 mycobacterium
p13257 methanosarcina
p50986 streptomyces o
Q9hkfl thermoplasma
085176 corynebacteriu
p57877 pasteurella mu
            059491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         097069 drosophila melanogasi
094354 schizosaccharomyces |
                                                                                                                 P08489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P14568 bos taurus (bovine)
                                                                                                                                                                                                                                                                          Q06734 streptomyces lavendu
P24532 streptomyces coelicol
                                                                                                                                                                                                                                                                                                                   P44315
P22767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p22768 saccharomyces cerevi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P16460 mus musculus (mouse)
                                                       P10387 triticum aestivum (WI
                                                                                                                                                                                                                                        P10162 homo sapiens
                                                                                                                                                                                                                                                           Q9ukn7 homo sapiens (human
                                                                                                                                     P54259 homo sapiens (human
P08489 triticum aestivum (w
                                                                                                                                                                                               P53420 homo sapiens (human
                                Q9qzz4 mus musculus (mouse)
                                                                                                                                                                                                                  62 homo sapiens (human).
epstein-barr virus (str
               lactococcus lactis
                                                                                                                                                                              rattus norvegicus (ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methanobacterium ther
                                                                                              homo sapiens
                                                                                                                    homo sapiens
                                                                                                                                                                                                                                                                                                                     escherichia coli.
                                                                                                                                                                                                                                                                                                                                    pasteurella multocida haemophilus influenza
                                                                                                                                                                                                                                                                                                                                                                                 corynebacterium glut
                                                                                                                                                                                                                                                                                                                                                                                                  streptomyces clavuli
thermoplasma acidoph
                                                                                                                                                                                                                                                                                                                                                                                                                                             methanosarcina barke:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mycobacterium tubercu
                                                                         triticum aestivum (w)
                                                                                                (human)
                                                                                                                    (human)
                   SwissProt_39:SMF1_HUMAN +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: SwissProt_39:ASSY_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SwissProt_39:EXTN_TOBAC
SwissProt_39:GLT5_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SwissProt_39:MGD1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SwissProt_39:S3A2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P00966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSY_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bock H.-G.O.,
"Sequence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 200-209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JIGASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Colon carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                           citrullinemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-90293089;
                                                                                                                                             Saheki I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131.
131.
131.
131.
```

```
21-JUI-1986 (Rel. 01, Created)
21-JUI-1986 (Rel. 01, Last Sequence update)
20-JUI-1986 (Rel. 40, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97295306; PubMed=9150948;
Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
"A two-dimensional gel database of human colon carcinoma proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Freytag S.O., Bock H.-G.O., Beaudet A.L., O'Brien W.E.; "Molecular structures of human argininosuccinate synthetase pseudogenes. Evolutionary and mechanistic implications."; J. Biol. Chem. 259:3160-3166(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A two-dimensional gel database c
Electrophoresis 18:605-613(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=84015388; PubMed=6194510;
BOCK H.-G.O., Su T.-S., O'Brien W.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kobayashi K., Jackson M.J., Tick D.B., O'Brien W.E., Beaudet A.L.; "Heterogeneity of mutations in argininosuccinate synthetase causing human citrullinemia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=84135824; PubMed=6321498;
                                                                                                                                                                                                                                                                                                                              "Mutations in argininosuccinate synthetase mRNA of Japanese patients, causing classical citrullinemia."; Am. J. Hum. Genet. 55:1103-1112(1994).
                                                           Enzyme Protein 48:251-264(1995).
-!- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE =
                                                                                                                                                                                                         Shaheen N:, Kobayashi K., Terazono H., Fukushige T., Horiuchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS THR-118; VAL-192; CYS-272; ARG-280; TRP-304 AND LEU-363.
MEDLINE-95067972; PubMed-7977368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kobayashi K., Rosenbloom C., Beaudet A.L., O'Brien W.E.; "Additional mutations in argininosuccinate synthetase causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92048472; PubMed=1943692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS S-14; H-157; N-180; S-324; W-304; W-363 AND R-390
                                                                                                                 synthetase proteins expressed in bacterial
                                                                                                                                                                                                                                         CHARACTERIZATION OF SOME VARIANTS.
MEDLINE=96385010; PubMed=8792870;
                                                                                                                                                                                                                                                                                                                                                                                                                      Kobayashi K., Shaheen N., Terazono H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS LEU-18 AND CYS-86.
                                                                                                                                                    "Characterization of human wild-type and mutant argininosuccinate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 265:11361-11367(1990).
PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                        PYROPHOSPHATE + L-ARGININOSUCCINATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Med. 8:95-100(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human argininosuccinate synthetase cDNA."; Res. 11:6505-6512(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=2358466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143.
141.
140.
138.
130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.5765
0.5832
0.5857
0.5954
0.6674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beaudet A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Saheki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA
                                                                                                                                       cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Q15428 homo sapiens (huma
1 Q9y573 homo sapiens (huma
1 P13983 nicotiana tabacum
1 P10388 triticum aestivum
1 O14497 homo sapiens (hum
```

```
SON TO SON THE PROPERTY OF THE
                                             alignment_block:
US-09-775-693-1 x ASSY_HUMAN
                                                                                                                                                                                    alignment_scores:
  Align seg 1/1 to: ASSY_HUMAN
                                                                                                                  Quality: 2144.00
Ratio: 5.204
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X01630; CAA25771.1; -.
EMBL; L00084; AAA51783.1; JOINED.
EMBL; L00080; AAA51783.1; JOINED.
EMBL; L00080; AAA51783.1; JOINED.
EMBL; L00081; AAA51783.1; JOINED.
EMBL; L00082; AAA51783.1; JOINED.
EMBL; L00083; AAA51783.1; JOINED.
EMBL; L00083; AAA51783.1; JOINED.
PIR; A01195; AJHURS.
MIM; 603470; -.
MIM; 603470; -.
                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; iPR001518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
Arginine biosynthesis; Urea cycle; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disease mutation.
NP_BIND 115
VARIANT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY.
SUBGUNIT: HOMOTETRAMER.
DISEASE: DEFECTS IN ASS ARE THE CAUSE OF CITRULLINEMIA, AN AUTOSOMAL RECESSIVE DISEASE CHARACTERIZED BY SEVERE VOMITING SPELLS AND MENTAL RETARDATION.
SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                    412 AA;
                                                                                                                                                                                                                                                                                                      390
                                                                                                                                                                                                                                                                                                                                                 363
                                                                                                                                                                                                                                                                                                                                                                                              363
                                                                                                                                                                                                                                                                                                                                                                                                                                           324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                                                                                                                                                                                                                                    390
                                                                                                                                                                                                                                                    46426 MW;
                                                                                                                                                                                                                                                                                                                                              363
                                                                                                                                                                                                                                                                                                                                                                                            363
                                                                                                                                                                                                                                                                                                                                                                                                                                         324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                                             Gaps:
Percent Identity:
    from: 1
                                                                                                                                                                                                                                                                                                                                /FTIG=VAR_000691.

R -> L (IN CITRULLINEMIA).
/FTIG=VAR_000692.

R -> W (IN CITRULLINEMIA).
                                                                                                                                                                                                                                                                                                                                                                                                                             G -> S (IN CITRULLINEMIA)
                                                                                                                                                                                                                                                                                        /FTId=VAR_000693.
G -> R (IN CITRULLINEMIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VAR_000688.
G -> R (IN CITRULLINEMIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL).
G -> S (IN CITRULLINEMIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VAR_000690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A -> V (IN CITRULLINEMIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A -> T (IN CITRULLINEMIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VAR_000689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_000687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR_000686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_000685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_000681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR_000683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VAR_000682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> W (IN CITRULLINEMIA)
                                                                                                                                                                                                                                               D9083E00655D0716 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> C (IN CITRULLINEMIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> N (IN CITRULLINEMIA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> H (IN CITRULLINEMIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> C (IN CITRULLINEMIA)
to: 412
                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IN CITRULLINEMIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _000684
                                                                                                             100.000
                                                                                                                                                          412
```

Page 3

SQ SQ

```
seq_name: SwissProt_39:ASSY_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1001 TCCGCCACTGCATCGCCAAGTCCCCAGGAGCGAGTGGAAGGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 GluTyrHisArgLeuGlnSerLysValThrAlaLys 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIGASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89016648; PubMed-3174461;
Surh L.C., Morris S.M., O'Brien W.E., Beaudet A.L.;
"Nucleotide sequence of the cDNA encoding the rat argininosuccinate
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its burden Bioinformatics Institute. There are no restrictions on its burden by an on-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY.
-!- SUBUNIT: HOMOTETRAMER
                                                                                                                                                                                                                                   -i- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                       EMBL; x12459; CAA30999.1; ...
EMBL; m35708; AAA40771.1; ...
PIR; S01440; AJRTRS.
Interpro; IPRO01518; Arginosuc_synth.
                                                                                                                or send an email to license@isb-sib.ch).
pfam; pr00764; Arginosuč_synth; 1.
probom; pb003544; Arginosuc_synth; 1.
proSITE; ps00564; ARGININOSUCCIN_SYN_1;
                                                                                                                                                                                                                                                                               PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus.
```

```
alignment_block:
US-09-775-693-1 x ASSY_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: ASSY_RAT from: 1 to: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    percent similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
Arginine biosynthesis; Urea cycle; Ligase; ATP-binding.
Arginine biosynthesis; Urea cycle; Ligase; ATP-binding.
123 ATP (POTENTIAL)
SEQUENCE 412 AA; 46496 MW; CCA80906F5A3E93D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGTCCAGCAAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                    251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                           351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTACT 400
                                                                                                                                                                                                                                                                              401 CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                             84 luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg 100
                                                                                                                                                                                                                                451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                      134 erLeuAlaProGlnileLysValIleAlaProTrpArgMetProGluPhe 150
                                                                                                                                                                                                       151 TyrasnargPheLysGlyargAsnaspLeuMetGluTyralaLysGlnHi 167
                                                                                                                                                             501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCATGGATGAGA 550
                                                                                                              551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC 600
                                                                 601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGGCCAAAGCCCC 650
                     651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700
701 AGGTGACCAACGTCAAGGATGGCACCACCCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 2086.00
                                                                                                                                                                                                                        րերինաննուրանարանարարարույն
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              percent Identity: 96.845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: SwissProt_39:ASSY_MOUSE
                                                                                          Gene 99:181-189(1991).
-!- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP +
-!- PATHMAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
-!- SUBUNIT: HOMOTETRAMER.
-!- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                MEDLINE=91216457; PubMed=1708740;
Surh L.C. Beaudet A.L., O'Brien W.E.;
"Molecular characterization of the murine argininosuccinate
synthetase locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P16460;
P16460;
P16460;
P1-AUG-1990 (Rel. 15, Created)
P1-AUG-1990 (Rel. 15, Last sequence update)
P15-JUL-1999 (Rel. 38, Last annotation update)
P15-JUL-1999 (Rel. 38, Last annotation update)
P15-JUL-1999 (Rel. 38, Last annotation update)
P16460;
P164600;
P1646000;
P1646000;
P1646000;
P1646000;
P1646000;
P1646000;
P16
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-DBA/2J; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASSY_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 GluTyrHisArgLeuGlnSerLysValThrAlaLys 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 luProlleAspAlaThrGlyPhelleAsnIleAsnSerLeuArgLeuLys 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 uSerLeuTyrAsnGluGluLeuValSerMetAsnValGlnGlyAspTyrG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 ValSerVaiPheLysGlyGlnValTyrileLeuGlyArgGluSerProLe 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 alargHisCysTleAspLysSerGinGluargValGluGlyLysValGin 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   901 ACCATGGACCGCGAAGTGCGCAAAATCAAACAACCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 ThrMetAspArgGluValArgLysIleLysGlnGlyLeuGlyLeuLysph 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         851 CCCCAGGAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 hrProAlaGlyThrileLeuTyrHisAlaHisLeuAspIleGluAlaPhe 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   751 TTCATGTACCTGAACGAAGTCGCGGGCAATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 PheMetTyrLeuAsnGluValAlaGlyLysHisGlyValGlyArgIleAs 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
```

```
alignment_block:
US-09-775-693-1 x ASSY_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: ASSY_MOUSE from: 1 to: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity: 98.786
451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                          134 erLeuAlaProGlnTieLysValTleAlaProTrpArgMetProGluPhe 150
                                           401 CACTGGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                    117 yAlaThrGlyLysGlyAsnAspGlnValArgPheGluLeuThrCysTyrs 134
                                                                                                       351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                101 ArgGinValGluiieAiaGinArgGluGlyAlaLysTyrValSerHisGl
                                                                                                                                                                 301 AAACAAGTGGAAATCGCCCAGCGGGGGGGGGGGGGCCAAGTATGTGTCCCCACGG 350
                                                                                                                                                                                                         151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCACCAGGGA 200
                                                                                                                                                                                                                                                                                                 101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                               51 AlaLeuLysLeuGlyAlaLysLysValPherleGluAspValSerLysGl 67
                                                                                                                                                                                                                                                                                                                                                                                         34 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 rSercysileLeuValTrpLeuLysGluGinGlyTyrAspValIleAlaT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M31690; AAA37266.1; EMBL; M31692; AAB60707.1; EMBL; M31694; AAB60708.1; EMBL; M31693; AAB60708.1; JOINED EMBL; M31695; AAB60708.1; JOINED EMBL; M31702; AAB60706.1; FIR; JU0463; AJMSRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD: MGI:88090; ASS1
InterPro; IPR001518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00364; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
Arginine biosynthesis; Urea cycle; Ligase; ATP-binding.
APP BIND 115 123 ATP (POTENTIAL).
NP_BIND 115 123 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetSerSerLysGlySerValValLeuAlaTyrSerGlyGlyLeuAspTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.lsb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 2073.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 96.117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A8F3AFDDFBDAEF6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
```

```
seq_name: SwissProt_39:ASSY_BOVIN
                                                                                                           seq_documentation_block:
     BERRRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   501 CGGGATTCCCCATCCCGGTCACTCCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 sGlylleProlleProvalThrProLysSerProTrpSerMetAspGluA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                701 AGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                          1051 GTGTCCGTCCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        951 TGCTGAGCTGGTGTATACCGGTTTACCGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 hrProAlaGlyThrileLeuTyTHisAlaHisLeuAspIleGluAlaPhe 300
                                                                                                                                                                                                                                                                      1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                   1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                          1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                    367 uSerLeuTyrAsnGluGluLeuValSerMetAsnValGlnGlyAspTyrG 384
O1-JAN-1990 (Rel. 13, Created)
O1-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE LIGASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 GluTyrHisArgLeuGlnSerLysValThrAlaLys 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysvalThrAsnIleLysAspGlyThrThrArgThrThrSerLeuGluLeu 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \verb|pileValGluAsnArgPheIleGlyMetLysSerArgGlyIleTyrGluT|\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 334
                                                                                                                                                                                                                                         luProlleAspAlaThrClyPheIleAsnIleAsnSerLeuArgLeuLys 400
                                                                                                               412 AA.
```

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-775-693-1 x ASSY_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio: 5.059
Percent Similarity: 99.272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: ASSY_BOVIN from: 1 to: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dennis J.A., Healy P.J., Beaudet A.L., O'Brien W.E.; "Molecular definition of bovine argininosuccinate synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90046714; PubMed=2813370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in make by non-profit institutions as long as its content is in the content in the content in the content is in the content in the content in the content is in the content in the conte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prodom; PD00544; Arginosuc_synth; 1.

PROSTTE; PS00564; ARGININOSUCCIN_SYN_2; 1.

PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.

PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.

Arginine biosynthesis; Urea cycle; Ligase; ATP-binding.

Arginine biosynthesis; Urea cycle; Ligase; ATP-binding.

NP_BIND 115 123 ATP (POTENTIAL).

NP_BIND 115 123 ATP (POTENTIAL).

SECUENCE 412 AA; 46417 MW; 6F74C7F445EEODB86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M26198; AAA30388.1; -.
PIR; A33986; AJBORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00764; Arginosuc_synth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001518; Arginosuc_synth
                                                                                                                                                                                                                                                                                                           101 ATCTGGCCAACATTGGCCAGAAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                              151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                             51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                  34 yrLeuAlaAsnīleGlyGlnLysGluAspPheGluGluAlaArgLysLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                    51 AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspIleSerLysGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISEASE:
                                                         PATHWAY.
                                                                                                                                                                                                   Quality: 2069.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 AA; 46417 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFECTS IN ASS ARE THE CAUSE OF A BOVINE FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 95.388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
```

```
1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                      1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCCACT 1100
                                                                                                                                                                                                                                                 1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                                                                                                                                   351 ValSerValPheLysGlyGlnValTyrileLeuGlyArgGluSerProLe 367
                                                                                                                                                                                                            334 alArgHisCysIleAlaLysSerGlnGluArgValGluGlyLysValGln 350
                                                                                                                                                                                                                                                                                     317 ealagluLeuvalTyrThrGlyPheTrpHisSerProGluCysGluPhev 334
                                                                                                                                                                                                                                                                                                                           951 TGCTGAGCTGGTGTATACCGGTTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                301 ThrMetAspArgGluValArgLysIleLysGlnGlyLeuGlyLeuLysPh 317
                                                                                                                                                                                                                                                                                                                                                                                                      901 ACCATGGACGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                           284 hrProAlaGlyThrfleLeuTyTHisAlaHisLeuAspIleGluAlaPhe 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               851 CCCCAGCAGGCACCATCGTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 prievalGluAsnArgPherleGlyMetLysSerArgClyTleTyrGluT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 PheLeuTyrLeuAsnGluValAlaGlyLysHisGlyValGlyArgIleAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 ysvalrhrasnvalGlyAspGlyThrThrHisSerThrAlaLeuGluLeu 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              701 AGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 oAsnSerProAspMetLeuGluIleGluPheLysLysGlyValProValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 GlnalaProProGlyLeuTyrThrLysThrGlnAspProAlaLysAlaPr 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 snLeuMetHisIleSerTyrGluAlaGlyIleLeuGluAsnProLysAsn 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 501 CGGGATTCCCATCCCGGTCACTCCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 TyrasnargPheGlnGlyArgAsnaspLeuMetGluTyralaLysGlnHi 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 erLeualaProGlnTleLysValIlealaProTrpArgMetProGluPhe 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 yAlaThrGlyLysGlyAsnAspGlnIleArgPheGluLeuThrCysTyrS 134
351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 AAACAAGTGGAAATCGCCCAGCGGGGGGGGGGGGCCAAGTATGTGTCCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysTleAlaArg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sGlyIleProValProValThrProLysAsnProTrpSerMetAspGluA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMBHIRMANTALIA
```

```
Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Addms M.D., Celniker S.E., Lil. W., Hoskins R.A., Galle R.F., RA Addms M.D., Celniker S.E., Lil. W., Hoskins R.A., Galle R.F., RA Addms M.D., Changer M., Henderson S.N., RA Sutcop G.G., Government M., Henderson S.N., RA Sutcop G.G., William J.F., Vandell M.D., Zhang G., Chen L.Y., RA Ballew R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mithos G.L.G., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mithos G.L.G., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M., Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M., Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M., Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M., Botchan M.R., Bouck J., Bayraktaroglu L., Bastey E.M., Borkova D., Daylas D., Lakas D., Daylas 
                         Seq_documentation_block
ID ASSY_DROME STAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: SwissProt_39:ASSY_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             097069; 09VI41;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete sequence of the Antennapedia complex of Drosophila.", Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Celniker S.E., Pfeiffer B., Knafels J., Martin C.H., Mayeda C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASPARTATE LIGASE).
BG:DS00004.14 OR CG13633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 GluTyrHisArgLeuGlnAsnLysValThrAlaLys 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 luProValAspAlaThrGlyPheIleAsnIleAsnSerLeuArgLeuLys 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
```

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-775-693-1 x ASSY_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 1164.00
Ratio: 3.571
Percent Similarity: 80.494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: ASSY_DROME from: 1 to: 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation on its the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute as its content is in no way the by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE001574; AAD19816.1; ALT_SEQ.
EMBL; AE003674; AAF54103.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prodom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_2; 1.
PROSITE: PS00565; ARGININOSUCCIN_SYN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0026565; BG:DS00004.14.
InterPro; IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arginine biosynthesis; urea cycle; Ligase; ATP-binding.
NP_BIND 114 122 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pfam; PF00764; Arginosuc_synth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 ACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCAT 59
                                                                                                                                                                                                                                                                                                                                                                                                                   160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 lLeuLysTrpLeuLeuAspLysGlnTyrGluValIleCysValLeuAlaA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 CCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCA 109
                                                                                                                                                                                                                                                                                                                                                   210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 spValGlyGlnLysGluAspPheThrAlaAlaGluLysLysAlaLeuLys 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LysGluThrValIleLeuAlaTyrSerGlyGlyLeuAspThrSerCysVa 19
                                                                                                                                                                                                                                                                               260 ACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                  53 IleGlyAlaLysLysValIleValAlaAspValLysGlnSerPheValGl 69
                                                                                                                                                                                                          310 GAAATCGCCCAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGG 359
                                                                                                                                        360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                         103 GluvalalaargGluTyrGlyalaLysTyrLeualaHisGlyalaThrGl 119
                                                                                                                                                                                                                                                                                                                  69 uAspTyrIleTrpProAlavalGinMetGlyLeuValTyrGluGluArgT 86
                                                  410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                     460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                   roAspLeuLysIleIleAlaproTrpArgAspValGluPheCysCysGln 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46594 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         percent Identity: 54.321
```

```
510 CATCCCGGTCACTCCCAAGAACCCGTGGAGGATGGATGAGAACCTCATGC 559
                                                                                                                                       seq_name: SwissProt_39:ASSY_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             560 ACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 uvalSerAlaLysProAlaThrProTrpSerThrAspAlaAsnIleLeuH 186
                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           610 CCAGGTCTCTACACGAAGACCCAGGACCCA...GCCAAAGCCCCCAACAC 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 isileSerTyrGluSerGlyIleLeuGluAspProAsnThrValAlaPro 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 GluAsnLeuTyrGluMetThrValAspProLeuThrArgAlaProArgAs 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 pProValHisLeuVallieGlnPheAspArgGlyLeuProSerSerVaiG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             657 CCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGAAGGTGA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              707 CCAACGTCAAGGATGGCACCACCCACCAGACGTCCTTGGAGCTCTTCATG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 luAspLeuProGlyGlyArgValTyrThrLysProLeuGluMetLeuAsp 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 PheLeuAsnLysLeuGlyGlySerTyrGlyIleGlyArgIleAspIleVa 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            757 TACCTGAACGAAGTCGCGGGCCAAGCATGGCGTGGGCCGTATTGACATCGT 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            807 GGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAG 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 IGluAsnArgPheValGlyLeuLysSerArgGlyValTyrGluThrProG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            857 CAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1007 ACTGCATCGCCAAGTCCCAGGAGCGAAGGGAAAGGGAAAGTGCAGGTGTCC 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 lyGlyThrIleLeuPheAlaAlaHisGlnAspLeuGluValPheAlaLeu 302
                                                                                                                                                                                                                                                                                                                                                                                                            1057 GTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTG..... 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           957 GCTGGTGTAFACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCC 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 AspargGluValLeuArgThrLysGlnValLeuArgAspArgMetAlaAs 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             907 GACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGA 956
                                                                                                                                                                                                                                                                                                                                       1102 ....TCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATT 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 pTyrValTyrAsnGlyPheTrpPheSerProGluAlaIleTyrAlaArgi 336
                                                                                                                                                                                                                                                                                                                                                                                                                                            1148 ATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCCTCAGGCTG 1197
                                                                                                                                                                                                                                                                                                         353 LeualaProGlyTyrCysArgAlaIleAlaArgLysAlaAlaLysAspVa 369
                                                                                                                                                                                                           1198 AAGGAATATCATCGT 1212
                                                                                                                                                                                                                                       386 yrvalProGinAspAlaGlyGlyPheIleAlaileAsnAlaValArgIle 402
                                                                                                                                                                          403 ArgGluHisValArg 407
           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                             ASSY_SCHPO
LIGASE).
                                                                                                     STANDARD;
                                                                                                              PRT;
                                                                                                                   410 AA
```

```
alignment_block:
US-09-775-693-1 x ASSY_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: ASSY_SCHPO from: 1 to: 410
                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity: 81.013 Percent Identity: 54.430
322 CGGGAGGGGCCAAGTATGTGTCCCACGGGGCCCACAGGAAAGGGGAACGA 371
                                                               272 CCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCCCAG 321
                                      92 hrSerLeuAlaArgProIleIleAlaArgArgGinIleGlnIleAlaGlu 108
                                                                                                              222 GCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACCTCCTGGGCA 271
                                                                                                                                                              172 AAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGAGTTCATCTG 221
                                                                                      75 eProAlaAlaGlnAlaAsnAlaIleTyrGluAsnValTyrLeuLeuGlyT 92
                                                                                                                                                                                                                 122 AGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGGGCCAAA 171
                                                                                                                                        59 LysvalTyrvalGiuAspLeuArgGluGluPheIleAsnAspThrValII 75
                                                                                                                                                                                         42 luGluAspTrpAspAlaAlaArgGluLysAlaLeuLysValGlyAlaLys 58
                                                                                                                                                                                                                                        25 urleGluGluGlyTrpGluValrieCysTyrMetAlaAsnValGlyGlnG 42
                                                                                                                                                                                                                                                          72 GAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTGGCCAGA 121
                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lyne M., Rajandream M.A., Barrell B.G., Baker S., Mungall K.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP +
PYROPHOSPHATE + L-ARGININOSUCCINATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungl: Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 1083.00
Ratio: 3.384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1B3B873A4DCD0C21 CRC64;
```

***	rMetArgLeuArg 401	.66	357 ASAVALTECTEGGECEGGAGTECCCACTGTCTCTCTACAATGA 11 357 ASAVAlThrvalLeuGlyArgLysSerAspThrAlaHisLeuTyrAspG1 37.	1019 AGTCCAAGAGCGAGTGGAAGGGAAAGTGCAAGGGTCCTCAAGGC 1068 340 alserGlngluvalvalAsnGlyvalValLysLeuSerValTyrLysGly 356	**************************************	ORANGE CONTROL OF THE PROPERTY	 273 rGlyLeuLysSerArgGlyCysTyrGluThrProGlyLeuThrIleLeuA 290	257 AlaArgArgAsnGlyValGlyArgIleAspIleValGluAsnArgPheSe 273	241 lyThrPheSerGlyValValSerIlePheTyrGlnLeuAsnAlaIle 256	225 rlleHispheGluLysGlyAlaProThrLysLeuGluCysLysAspG 721 722 GCACCCACCACACCACACCTCACCACGATCATC 722 GCACCCACCACCACACACACACACATCACCACCACCACCAC	209 LysLeuThrvalAspProLysAspAlaProAspGluValGluGluLeuSe 225	192 lualaciyileLeuGluAspArccaAGAACCAAGCGCCTCCAGGTCTCTAC 621 192 lualaciyileLeuGluAspProSerMetThrProProLysAspMetTrp 208 622 ACGAAGACCCAAGGACCCAGCCAAACCCCAGGCTAAACCCCAGGACCCAAGACCCAAGACCAAACCCAAGACCAAACCCCAGCCAAACCCCAGGCAAACCCCAAGACCAAACCCCAGGCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAACCCCAAGACCAAAACCCCAAGACCAAAACCCAAGACCAAAACCCCAAGACCAAAACCCCAAGACCAAAACCCCAAGACCAAAACCCAAAACCCAAGACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAA	175 rThrLysLysProTrpSerMetAspGluAsnIleValHisCysSerTyrG 192 572 AGGCTGGAATCCCCACACCACCACCACCACCACCACCACCACCACCA	- ANTI-MCUTGATGGAGTACGCAAAGCAACACGGGATTCCCCATCCCGGTCAC 52 59 LysAspLeuLeuGluTyrAlaalaalaLysGlyTleProValThrGlnTh 17: 22 TCCCAAGAACCCCTCC	- CALLOCTCCCTGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCCC	. 42	LysGluAsnCysIleAlaValSerHisGlyCysThrGlyLysGlyAsnAs 12

seq_documentation_block:

Page 9

```
ASSY_YEAST STANDARD; PRT; 420 AA.
P22768;
P22768;
P3.405-1991 (Rel. 19, Created)
P3.405-1996 (Rel. 34, Last sequence update)
P3.505-1999 (Rel. 38, Last annotation update)
P3.405-1999 (Rel. 38, Last annotation update)
P4.505-1999 (Rel. 38, Last annotation update)
P5.505-1999 (Rel. 38, Last annotation update)
P6.505-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIGASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakamura Y., Baumberg S., Glansdorff N.; "Sequences of the genes encoding argininosuccinate synthetase in Escherichia coli and Saccharomyces cerevisiae: comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    van Vliet F., Crabeel M., Boyen A., Tricot C., Stalon V., Falmagne P., Nakamura Y., Baumberg S., Glansdorff N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-91071613; PubMed=2123815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 methanogenic archaebacteria and mammals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mannhaupt G., Vetter I., Schwarzlose C., Mitzel S., Feldmann H.; "Analysis of a 26 kb region on the left arm of yeast chromosome XV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96381248; PubMed=8789261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 95:99-104(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crabeel M., Seneca S., Devos K., Glansdorff N.;
"Arginine repression of the Saccharomyces cerevisiae ARG1 gene.
Comparison of the ARG1 and ARG3 control regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-57 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast 12:67-76(1996).
                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its buropean Bioinformatics Institute. There are no restrictions on its buropean Bioinformatics Institutions as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modifies and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/entities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                          EMBL; M35237; AAA34437.1; ...
EMBL; X91067; CAA62528.1; ...
EMBL; Z74800; CAA99067.1; ...
EMBL; X07070; CAA30106.1; ...
                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                 ProDom; PD003544; Arginosuc_synth; 1.
PROSTTE; PS00564; ARGININOSUCCIN_SYN_1; 1.
                                                                                                                                                                                                     Pfam; PF00764; Arginosuc_synth;
                                                                                                                NP_BIND
                                                                                                                               Arginine biosynthesis; Urea
                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OR YOL058W OR 01228.
                                      CONFLICT
                                                          CONFLICT
      SEQUENCE
                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYROPHOSPHATE + L-ARGININOSUCCINATE

CAPTABOLIC FUNCTION SINCE IT
FUNCTION: IN YEAST, AS CAN HAVE A CATABOLIC FUNCTION SINCE IT
FUNCTION: IN YEAST, AS CAN HAVE A CATABOLIC FUNCTION SINCE AND THE ARGINASE PATHWAY.

REACTIONS INVOLVED IN THE ARGININSS PATHWAY.

CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE - AMP +
CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE - AMP +
PYROPHOSPHATE + L-ARGININOSUCCINATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY
                                                                                                                                                                                                                                           S0005419;
                                                                                                                                                                                                                                                                  JQ0779; AJBYRS
                                                                                                                                       pS00565; ARGININOSUCCIN_SYN_2; 1.
blosynthesis; Urea cycle; Ligase; ATP-binding.
                                                                                                                                                                                                                           15419; ARG1.
IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / FY73;
            420 AA;
              46939 MW;
                              GY -> AT (IN REF. 1 AND 3).

EX -> VL (IN REF. 1 AND 3).

EX -> VC (IN REF. 1).

VDCR -> GGLS (IN REF. 1).

P -> F (IN REF. 1).

F -> L (IN REF. 1).
                                                                                                                         ATP (POTENTIAL)
                7E53C9DD58443860 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            420 AA
```

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-775-693-1 x ASSY_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio: 3.351 percent similarity: 77.053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: ASSY_YEAST from: 1 to: 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 CCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 AAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 GGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 lIleLeuAlaTrpLeuLeuAspGinGlyTyrGluValValAlaPheMetA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 CATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 IleAspValAlaLysGlnGluGlyCysPheAlaValSerHisGlyCysTh 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 GTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 GCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 laAsnValGlyGlnGluGluAspPheAspAlaAlaLysGluLysAlaLeu 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AGCAAAGGCTCCGTGGTTCTGGGCCTACAGTGGCGGCCTGGACACCTCGTG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 LysileGlyAlaCysLysPheValCysValAspCysArgGluAspPheVa 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 rGlyLysGlyAsnAspGinIleArgPheGluLeuSerPheTyrAlaLeuL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 ILYSASpIleLeuPheproAlaValGinValAsnAlaValTyrGiuAspV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                 135 ysProAspValLysCysIleThrProTrpArgMetProGluPhePheGlu 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407 CCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAAC 456
                                                                                                                                                                                                                                                                                                                                    507
                                                                                                                                                                                                                                  557 TGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCG 606
                                                                                                                                                                                                                                                                                                  168 eProValalaGlnThrLysAlaLysProTrpSerThrAspGluAsnGlnA 185
                                                                                                                                                                                                   607 CCTCCAGGTCTCTACACGAAGACCCAGGACCCAACCCCAACAC 656
                                                                                                                               657 CCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCCTGTGAAAGGTGA 706
                                                                                                218 nProGlnAspLeuThrileAspPheGluArgGlyLeuProValLysLeuT 235
745 GAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCG
                                235 hrTyrThrAspAsoLysThrSerLysGluValSerValThrLysProLeu
                                                                 707 CCAACGTCAAGGATGGCACCACCACCAGACCTCC......TTG 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 1069.00
                                                                                                                                                                                                                                                                                                                                   TCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCA 556
                                                                                                                                                                                                                                                                                                                                                                                                    CGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGAT 506
                                                                                                                                                                  ProLysAspMetTrpLysLeuIleValAspProMetAspAlaProAspGl 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       percent Identity: 50.483
```

```
RA MEDINE-2008/488; PubMed-10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Mayer K.F.X., Schueller C., Wambutt R., Entian K.-D., Terryn N.,
RA Harris B., Ansorge W., Brandt P., Grivell L., Rieger M.,
RA Weichselgarrner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Lanjham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Watsenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Mooljman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Mooljman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berneiser S., Hempel S., Feidpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: SwissProt_39:ASSY_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress), Eukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARGININOSUCCINATE SYNTHASE, CHLOROPLAST PRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AT4G24830 OR F617.40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1189 CTCAGGCTGAAGGAATATCATCGTCTCCAGAGCAAGGTCACT 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CITRULLINE -- ASPARTATE LIGASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1139 AGGGTGATTATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCC 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9SZX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASSY_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402 IleArgIleLysLysTyrGly.....GluSerLysLysThr 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1092 GTCCCCACTG...TCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGC 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 euThrGlyPheLeuProThrAspThrThrGlyPheIleAlaIleGlnAla 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1042 AAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGA 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 rThrLysThrGluLysLeuTyrAspProThrGluSerSerMetAspGluL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 ThrvalArgValArgLeuTyrLysGlyAsnValIleIleLeuGlyArgSe 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335 ysGluTyrIleArgSerMetIleGlnProSerGlnAsnSerValAsnGly 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          992 GTGAATTTGTCCGCCACTGCATCGCCAAGTCCCCAGGAGCGAGTGGAAGGG 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 rProAsnTyrSerArgLeuIleTyrAsnGlyPheLeuLeuHisProGluC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   942 CTTGAAATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGT 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 GlyLeuThrLeuAspLysGluValArgGlnLeuArgAspSerPheValTh 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     895 GCCTTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGC...CTGGG 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 yrGluGlnAlaproLeurhrValLeuArgLysAlaHisValAspLeuGlu 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              845 ACGAGACCCCAGCAGCCACCATCCTTTACCATGCTCATTTAGACATCGAG 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   795 TATTGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCT 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 ASPValPheLeuAlaAlaSerASnLeuAlaArgAlaAsnGlyValGlyAr 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gīleAspīleValGluAspArgTyrīleAsnLeuLysSerArgGlyCysT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          annotation update)
CHLOROPLAST PRECURSOR (EC 6.3.4.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              523 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       core eudicots; Rosidae;
```

```
alignment_block:
                                                                                                                                                                                                                                                             alignment_scores;
US-09-775-693-1 x ASSY_ARATH
                                                                     Quality: 911.50
Ratio: 3.018
Percent Similarity: 76.263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RA Schnabl S. Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habernann K.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habernann K.,
RA Schkon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Scheking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Scheking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante N., Geots I., Layman D.,
RA Melson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Mandoul B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaugnessy A., Rodriquez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RT Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               EMBL; AL049657; CAB41123.1; ALT_SEQ.
EMBL; AL161562; CAB79393.1; ALT_SEQ.
InterPro; IPR001518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                           TRANSIT
                                                                                                                                                                                                                                                                Arginine biosynthesis; Llgase; ATP-binding; Transit peptide;
                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CHLOROPLAST (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
-!- CAUTION: REF. 1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO WRONG EXON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished observations (JUN-2001).

-I- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP + PROPHOSPHATE + L-ARGININOSUCCINATE.

-I- PATHWAY: PENULTIMATE STEP IN ARGININE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONCEPTUAL TRANSLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 402:769-777(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S., Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., Pettett A., Rajandream M.-A., Lyne M., Benes V., Rechmann S., Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H., Dose S., de Haan M., Maarse A., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E., Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R., Schnahl S. Hillar B. Schmidt G. Muendlein A., Felber R., Schnahl S. Hillar B. Schmidt G. Muendlein A., Felber R.,
                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                 ; PD003544; Arginosuc_synth; 1.
E; PS00564; ARGININOSUCCIN_SYN_1; 1.
E; PS00565; ARGININOSUCCIN_SYN_2; 1.
                                                                                                                                                                                                         523 AA;
                                                                                                                                                                                               523 AI
; 57249 MW;
                                                    Percent Identity: 45.707
                                                                                                                                                                                                      CHLOROPLAST (POTENTIAL).
ARGININOSUCCINATE SYNTHASE.
                                                                                                                                                                                   97B82A5A718969C8 CRC64;
```

```
Align seg 1/1 to: ASSY_ARATH from: 1 to: 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 valvalLeuAlaTyrSerGlyGlyLeuAspThrSerValIleValProTr 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 pLeuLysGluAsnTyrGlyCysGluValValCysPheThrAlaAspValG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 GCCAGAAG...GAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 iydinGlyTleLysGluLeuGiuGlyLeuGluGlnLysAlaLysAlaSer 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 GlyalaSerGlnLeuValValLysAspLeuThrGluGluPheValLysAs 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 pPheilePheProCysLeuArgAlaGlyAlaIleTyrGluArgLySTyrL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 TCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 ATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 euLeuGlyThrSerMetAlaArgProValIleAlaLysAlaMetValAsp 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 ValalaalaGluValGlyAlaAspAlaValalaHisGlyCysThrGlyLy 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413 AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 GlnGlyArgGluAspAlaIleGluTyrAlaLysLysHisAsnValProVa 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCAT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                       513 CCCGGTCACTCCCAAGAACCCGTGGAGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                                                                                                                                        290 lProvalThrLysLysSerIleTyrSerArgAspArgAsnLeuTrpHist 307
                                                                                                                                                                                                                                                                                                                                                                                        563 TCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                                                                                                                         613 GGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCCTGA 662
                                                                                                                                                                                                                                                          663 CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                                                                                                                                                                                                                                                           324 ASPMetTyrMetMetSerValAspProGluAspAlaProAspGlnProGl 340
                                                                                                                                                                                                                              340 uTyrileGluileGlyIleGluSerGlyLeuProValAlaLeuAsnGly. 356
                                                                                                                                                                                              713 TCAAGGATGGCACCACCAGACCTCCTTGGAGCTCTTCATGTACCTG 762
                                                                                                                  763 AACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAA 812
                              813 CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCA 862
                                                                                                369 AsnThrIleGlyGlyLysHisGlyIleGlyArgIleAspMetValGluAs 385
 863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG 912
                                                                                                                                                                                                                                                                                                                                                           euserHisGluGlyAspLeuLeuGluAspProAlaAsnGluProLysLys 323
                                                                                                                                                                 LysalaLeuSerProalaThrLeuLeuAlaGluLeu 368
```

```
seq_name: SwissProt_39:ASSY_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
402 hrIleLeuPheAlaAlaValGinGluLeuGluSerLeuThrLeuAspArg 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1063 AAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCCACTGTCTCTCTACAA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               963 GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 GiuSerrieGlnValLysAspThrLeuAlaLeuLysTyrAlaGluMetVa 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    913 GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435 lTyralaGlyArgTrpPheAspProLeuArgGluSerMetAspAlaPheM 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1113 TGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 etGluLys1leThrGluThrThrGlySerValThrLeuLysLeuTyr 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1163 CCACCGGGTTCATCAACATCAATTCCCTCAGGGTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            469 LysGlySerValSerValThrGlyArgGlnSerProAsnSerLeuTyrAr 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          485 gGlnAspIleSerSerPheGluGlySerGluIleTyrAsnGlnAlaAspA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     502 laAlaGlyPheileArgLeuTyrGlyLeuProMetLys 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASSY_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and function of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bactleria; Firmicutes; Bacillus/Clostridium group; Bactlus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIGASE) ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=98048467; PubMed=9387221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1423
                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation its between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no terrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - PATHWAY: PENULTIMATE STEP IN ARGININE BIOSYNTHESIS.
- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                  entitles requires a license agreement (% or send an email to license@isb-sib.ch).
      pfam; PF00764; Arginosuc_synth; 1.
proDom; PD003544; Arginosuc_synth; 1.
proDom; PD003544; Arginosuccin_syn_1; 1.
pROSITE; PS00564; ARGININOSUCCIN_SYN_2; 1.
pROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.
Arginine biosynthesis; Ligase; BFF522A77386111F CRC64;
SEQUENCE 403 AA; 44817 MM; BEF522A77386111F
                                                                                                                                                                                                                                                EMBL; Z99119; CAB14923.1; -. EMBL; Z99118; CAB14905.1; -.
                                                                                                                                                                                    SubtiList; BG12570; argG.
InterPro; IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                            AF008220; AAC00320.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                 license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403 AA
```

```
751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                             229 erile.....AspGlyValSerTyrSerLeuSer...GluLeu 240
                                                            701 AGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTC 750
                                                                                             212 oAspThrProGluValIleGluILeAlaPheGluGlnGlyValProValS 229
                                                                                                                           651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                      601 CAAGCCCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC 650
                                                                                                                                                        196 AlaProProGluGlyAlaTyrAspLeuThrAlaProLeuGluLysThrPr 212
                                                                                                                                                                                                                     ||||||
179 snLeuTrpGlyArgAlaAsnGluCysGlyIleLeuGluAspFroTrpAla 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-775-693-1 x ASSY_BACSU
                                                                                                                                                                                                                                                  551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAAC 600
                                                                                                                                                                                                                                                                                  162 gGlyTleProTleProTleAsnLeuAspSerProTyrSerTleAspGlnA 179
                                                                                                                                                                                                                                                                                                             501 CGGGATTCCCCATCCCGGTCACTCCCCAAGAACCCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                           151 .....SerArgGluGluGluIleGluTyrAlaAlaSerAr 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: ASSY_BACSU from: 1 to: 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                          451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                         134 erLeuAsnProAspLeuGluValīleAlaProValArgGluTrpGlnTrp 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 818.00
Ratio: 2.773
Percent Similarity: 73.750
                                                                                                                                                                                                                                                                                                                                                                                                                                       401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 yCysThrGlyLysGlyAsnAspGlnValArgPheGluValSerIleLysS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 GGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 AAACAAGTGGAAATCGCCCAGGGGGGGGGGGGGCGAAGTATGTGTCCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 luGlyLysTyrProLeuValSerAlaLeuSerArgProLeuIleAlaLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 uPheAlaGlnAspTyrAlaLeuIleSerLeuGlnAlaHisThrMetTyrG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 GCACTGAAGCTTGGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AlaLeuGluValGiyAlaThrAsnSerTyrValIleAspAlaLysGluGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 ysCysLeuAspValGiyGluGlyLysAspLeuAlaPheValGInGlnLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 rServalAlaTleLysTrpLeuGlnGluGlnGlyTyrAsnValIleAlac 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetSerGluGlnLysLysValValLeuAlaTyrSerGlyGlyLeuAspTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 42.750
```

```
AC STRAIN-TOKYO 1998.

AX MEDLINE-20.445173; PubMed=10993077;
AS Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Telenome sequence of the endoceilular bacterial symbiont of aphids CC PATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP + CC PYROPHOSPHATE + L-ARGININOSUCCINATE

CC PATHAXY: PERULTIMATE STEP IN AGGININE BIOSYNTHESIS.

CC -I- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

CC -I- SUBUNIT: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: SwissProt_39:ASSY_BUCAI
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                       Symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                    Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASSY_BUCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 sphishisAlaAlaTleGlyPheTleGluLeuTrpGlyLeuProThrLys 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1051 GTGTCCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 rSerLeuTyrAspGluLysLeuAlaThrTyrThrLysAspAspAlaPheA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341 vaiLysLeupheLysciyHisAlaIleValGluciyArgLysSerGluTy 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 euHisAlaPheLeuLysGluThrGlnLysHisValThrGlyTleValArg 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 tSerGluIleIleTyrAsnGlyLeuTrpPheSerProLeuLysAspAlaL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 ThrLeuValLysGluValAlaHisPheLysProIleIleGluGlnLysMe 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           901 ACCATEGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 ysproGlyAlaMetThrLeuIleLysAlaHisLysGluLeuGluAspLeu 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        851 CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 pHisValGluAsnArgLeuValGlyIleLysSerArgGluValTyrGluC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       403 AA
```

```
DR
DR
DR
DR
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-775-693-1 x ASSY_BUCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: ASSY_BUCAI from: 1 to: 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prodom: PD003544; Arginosuc_synth; 1.

PROSITE: PS00564; ARGININOSUCCIN_SYN_1; 1.

PROSITE: PS00565; ARGININOSUCCIN_SYN_2; 1.

Arginine biosynthesis; Llyqase; ATP-binding; Complete proteome.

BEQUENCE 403 AA; 45072 MW; F23B7024C8BDB147 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR001518; Arginosuc_synth. pfam; PF00764; Arginosuc_synth; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 GCCAG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 GGGCCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                           413 AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 sGlyAsnAspGlnValArgPheGluMetAlaTyrAlaAlaLeuAlaProA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 ATCGCCCAGCGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 TCCTGGGCACCTCTTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 lyGlnSerLysLysAspLeuAsnGlyIleGluLysLysSerLeuGluSer 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 pLeuLysGluAsnTyrAsnPheGluValValAlaPheValAlaAspIleG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 nTyrValTyrProValLeuLysThrGlyAlaLeuTyrGluGlySerTyrL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 snLeuAsnValIleAlaProTrpArg.....GluTrp.....AsnLeu 154
                                                                                                                                                                                                                                                                                                                                                       463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCAT 512
                                                                                                                                            188 leSerThrGluGlyGlyLeuLeuGluAsnProTrpAsnGlnSerAsnGlu 204
                                                                                                                                                                                    563 TCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                             171 rThrAlaThrLeuGluLysIleTyrSerLysAspGluAsnSerTrpHisI 188
                                                                                                                                                                                                                                                                    513 CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                              155 AsnSerArgGluSerLeuLeuLysTyrLeuAspLysLysAsnIleSerTh 171
                                                                                                 613 GGTCTCTACACGAAGACCCAGGACCCAGCCCAAAGCCCCCAACACCCCCTGA 662
                  663 CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                          205 AspCysTrpSerTrpThrValAsnProGluAspAlaProGluLysProGl 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           euLeuGlyThrAlaMetAlaArgProIleIleAlaLysLysGlnValGlu 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
..........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              807.50
2.710
75.253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 43.687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
```

```
seq_name: SwissProt_39:ASSY_AQUAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           713 TCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATGTACCTG 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 uTyrValSerLeuGlnLeuLysGluGlyCysValValSerValAsnAsnG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 lnLys.....LeuAsnProLeuLysCysValGluGluLeu 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1063 AAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 nArgLeuIleGlyMetLysSerArgGlyCysTyrGluThrProGlyGlyT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       813 CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAGCAGGCA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             763 AACGAAGTCGCGGGCAAGCATGGCGTGGGGCCGTATTGACATCGTGGAGAA 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1113 TGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               913 GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 hrileIleMetThralaIleLysAlaIleGluGlnLeuValLeuAspArg 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1163 CCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 lTyrAspGlyArgTrpPheSerProIleArgLysSerLeuGlnAlaAlaA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     963 GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 GluSerPheArgTrpArgGluLysIleGlyLeuGluMetSerSerIleVa 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              333 laAspSerLeuSerLeuGluIleThrGlyGluValIleLeuLysLeuTyr 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 LysGlySerValThrAlaValGlnLysLysSerProAsnSerLeuTyrSe 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 rGluGluTyrAlaThrPheGlyGluAspLysValTyrLysGlnSerAspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSY_AQUAE STANDARD; PAL, TO CONTROL OF CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 laAspGlyPheIleArgLeuPheSerLeuSerSerLys 395
                                                                                                                                                                                                                                                                                                              Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Aquificales; Aquificaceae; Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIGASE).
                                                                 NATURE 392:353-358(1998).

NATURE 392:353-358(1998).

PATRALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP + CATRALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE.

PYROPHOSPHATE + L-ARGININOSUCCINATE.

PATHWAY: PENULTIMATE STEP IN ARGININOSUCCINATE SYNTHASE FAMILY.

SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARGG OR AQ_1140.
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: ASSY_AQUAE from: 1 to: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-775-693-1 x ASSY_AQUAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
         560 ACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCAGCCCT 609
                                                   165 oVallysalaThrLysGluLysProTyrSerIleAspArgAsnLeuTrpG 182
                                                                                             510 CATCCCGGTCACTCCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGC 559
                                                                                                                                                                   460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                         149 PheLysSerArgGluGluGlnValGluTyrAlaGlnArgPheAsnIlePr 165
                                                                                                                                                                                                                           136 roAspileGluValLeuAlaProValArgGluTrpGlu...... 148
                                                                                                                                                                                                                                                                       410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                                 119 yLysGlyAsnAspGlnValArgPheGluLeuSerValTrpAlaLeuAsnp 136
                                                                                                                                                                                                                                                                                                                                                           360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                                   103 TyrTyralaGluLysPheAsnalaAspTyrValAlaHisGlySerThrGl 119
                                                                                                                                                                                                                                                                                                                                                                                                                                               310 GAAATCGCCCAGCGGGAAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 ACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 yrProLeuThrAlaAlaLeuSerArgProLeuIleAlaGluArgLeuVal 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 ACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCCACTGAAG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 uAsnTyrCysLeuProThrLeuArgAlaLeuAlaLeuTyrGluGlyLysT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 AlaGiyAiaTleGluAlaTleValGluAspLeuLysGluThrPheAlaGl 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 spValGlyGlnGlyGluGluLeuSerGluIleProGluLysAlaArgArg 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 eValargTrpLeuThrGluLysGlyTyrGluValIleThrTyrThrAlaA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.
SEQUENCE 401 AA; 45848 MW; 2BCBA9D027CE33CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 CCTCGTGTGGCTGAAGGAACAAGGCTAATGACGTCATTGCCTATCTGGCCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ANAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCAT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000725; AAC07170.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LysLysArgVailleLeuAlaTyrSerGlyGlyLeuAspThrSerIleil 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
H:::HH HHH:::HH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        800.50
2.741
72.277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 41.832
```

```
seq_name: SwissProt_39:ASSY_LACLA
                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
MEDLINE=21235186; PubMed=11337471;
                             SEQUENCE FROM N.A. STRAIN-IL1403;
                                                                                                                                                                                                    20-AUG 2001 (Rel. 40, Created)
20-AUG 2001 (Rel. 40, Last sequence update)
20-AUG 2001 (Rel. 40, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                 ARGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1207 CATCGTCTCCAG 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1157 CTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATAT 1206
                                                                                                   NCBI_TaxID=1360;
                                                                                                                                            Lactococcus lactis (subsp. lactis) (Streptococcus lactis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1107 CTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAA 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                              395 GlyArgValArg 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 leAlaGlyLysHisPheThrLysValTrpGlyLeuProLeuLysValLeu 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1057 GTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCT 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1007 ACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAAGGGAAAGTGCAGGTGTCC 1056
                                                                                                                                                                                                                                                                                                                                                   ASSY_LACLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 uTyrValGluGluLeuAlaThrTyrSerGluLysAspGlnPheAspGlnI 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345 LeuTyrLysGlySerValSerValGlyArgArgSerProAsnSerLe 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 laPheThrAsnLysIleAlaGluPheAlaThrGlyGluValArgLeuLys 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 sLeuValTyrGluGlyLeuTrpPheThrProLeuArgGluAlaLeuAspA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        957 GCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCC 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 ArgpheThrPheHisTyrPheLeuThrHisTleProHisGluTyrAlaLy 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               910 CGG...GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGA 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 laMetValLeuTyrGluAlaTyrArgAspLeuLeuSerLeuValLeuAsp 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    860 GCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGAC 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 uAsnargLeuValGlyIleLysSerArgGluIleTyrGiuAlaProGlyA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          810 GAACCGCTTCATTGGAATGAAGTCCCCGAGGTATCTACGAGACCCCCAGCAG 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 LeuAsnGluIleAlaGlyArgHisGlyValGlyArgileAspMetValGl 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                760 CTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 .....AsnGlyGluArgTyrGluGluGlnTrpLysLeuIleAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          710 ACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTCATGTAC 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 oGluTyrValThrValGlyPheGluLysGlyLysProValTyrLeu.... 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               660 TGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGAAGGTGACCA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 GlnAspAlaTyrGlnIleThrGlnSerProGluGluAlaProAspGluPr 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         610 CCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCC 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 lyValSerIleGluCysGlyProLeuGluAspProTrpGlnGluProPro 198
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                         398 AA
```

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: ASSY_LACLA from: 1 to: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-775-693-1 x ASSY_LACLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entitles requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001518; Arginosuc_synth.

Pfam; PF00764; Arginosuc_synth; 1.

ProDom; PD003544; Arginosuc_synth; 1.

PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.

PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.

Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.

SEQUENCE 398 AA; 43960 MW; 11411DF9C9274712 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE006250; AAK04222.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                84 luAsnLysTyrProLeuValSerAlaLeuSerArgProLeuIleAlaGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 AlaLeuGlnValGlyAlaValGluSerValValLeuAspCysLysGluGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 spCysMetAspValGlyGluGlyLysAspLeuAsnPheIleHisAspLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 rSerValAlaValLysTrpLeuThrAspLysGlyPheAspValIleAlaA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetMetGlyAsnLysLysIleValLeuAlaTyrSerGlyGlyLeuAspTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uPheAlaLysIlePheValGlyAlaAlaLeuLysGlyAsnLeuMetTyrG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                         yCysThrGlyLysGlyAsnAspGlnValArgPheGluValAlaIleHisS 134
                                                                                                                                                                                     CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                          {\tt LysLeuValGluValAlaLysGluLysGlyAlaThrAlaIleAlaHisGlusLeuValGluValAlaLysGluLysGlyAlaThrAlaIleAlaHisGlusLeuValGluValAlaLysGluLysGlyAlaThrAlaIleAlaHisGlusLeuValGluValAlaLysGluLysGlyAlaThrAlaIleAlaHisGlusLeuValGluValAlaLysGluLysGlyAlaThrAlaIleAlaHisGlusLeuValGluValAlaLysGluLysGlyAlaThrAlaIleAlaHisGlusLeuValGluValAlaHisGlusLeuValGluUValAlaHisGlusLeuValGluValAlaHisGlusLeuValGluUValAlaHisGlusLeuValGluValAlaHisGlusLeuValGluUValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAlaHisGlusLeuValAla
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               777.00
2.707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 41.117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
```

ARGG OR SLR0585

LIGASE)

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE

seq_name: SwissProt_39:ASSY_SYNY3

seq_documentation_block:

ASSY_SYNY3

STANDARD;

PRT;

400 AA

```
134 erLeuAlaProGluLeuGluValIleAlaProValArg......GluTrp 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501 CGGGATTCCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 His.....TrpAlaArgGluGluIleGluTyrAlaAsnGlnAs 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 nGlyValProIleProAlaAspLeuAspAsnProTyrSerIleAspMetA 179
                                                                                                                                                       1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                   1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 ThrCysProGluAspAlaPhePheMetThrAsnSerValGluAsnAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGGCCAAAGCCCC 650
                                                                                                                                                                                                                                                            1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 laLeu...AsnGlyLysSerLeuGluLeuHis......GluIle 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               701 AGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 oAsnGluAlaGluPheIleGluValGluPheLysGluGlyLeuProIleA 229
                                                  1151 AGCCAACTGATGCCACCGGGTTCATCAACATC 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             851 CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 ThrPheValArgGluLeuAlaHisPheLysProValLeuGluAsnGluLe 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 ysproAlaAlaIleThrLeuLeuLysAlaHisLysAspLeuGluAspLeu
                                                                                                                                                                                                         341 IleLysLeuTyrLysGlyLeuAlaThrProValGlyArgLysSerThrAs 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
374 spGlnAlaAlaValGlyPheIleLysLeu 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nSerLeuTyrSerGluLysLeuAlaThrTyrThrAlaAlaAspGluPheA 374
                                                                                                                                                                                                                                                                                                                 euIleAlaTyrLeuAspGluThrGlnLysValValAsnGlyIleValLys 340
                                                                                                                                                                                                                                                                                                                                                                                                                      uAlaAsnLeuIleTyrAsnGlyLeuTrpPheAsnProAlaThrLysAlaL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290
```

```
alignment_block:
US-09-775-693-1 x ASSY_SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: ASSY_SYNY3 from: 1 to: 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                       245 TGTATGAGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATC 294
                                                                                                                         195 CAGGGAGTTTGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCAC 244
                                                                                                                                                                                                           145 AAGAAGGCACTGAAGCTTGGGGCCAAAAAGGTGTCATTGAGGATGTCAG 194
                 84
                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prom; PF00764; Arginosuc_synth; 1.

Prodom; PD003544; Arginosuc_synth; 1.

PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.

PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.

Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.

Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.
                                                                                                                                                                   51 GluLysAlaLeuArgCysGlyAlaValGluSerLeuValIleAspGlyLy 67
                                                                                                                                                                                                                                                     34 leThrLeuAlaAlaAspLeuGlyGlnGlyAspGluLeuGlyProIleGln 50
                                                                                                                                                                                                                                                                                               95 TTGCCTATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGG 144
                                                                                                                                                                                                                                                                                                                                       17 rSerValCysIleProTyrLeuMetHisGluTrpGlyValGluGluValI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                              51 CTCG...TGCATCCTCGTGTGGCTGAAGGAACAAGGCTAT...GACGTCA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D90917; BAA18841.1; -.
InterPro; IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE - AMP + PYROPHOSPHATE + L-ARGININOSUCCINATE.
- PARHWAY: PENULTIMATE STEP IN ARGININE BIOSYNTHESIS.
- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97061201; PubMed=8905231; Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajina N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
euTyrGluAsnArgTyrProLeuSerThrAlaLeuAlaArgProLeuIle 100
                                                                                 sGluGluPheValLysGluTyrAlaPheArgSerIleGlnAlaAsnAlaL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3:109-136(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               764.00
2.709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 41.626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okumura S.,
```

7	353		22 88	933 303	80 80	7 3		4. 0	ຄົ 🌣	0 4	, io 6						
- 33 ⋯ (8 <u>- 5</u>	GTG Val	H _ C	AGG ; nTh	TTA Arg	e = c	sG TG	. CA	Ys - A	al	0-0	٠ o	9 aT) i o	1 4 5	7 5 a : 0	1
tG1	19 - 16 - 16 - 16 - 16 - 16 - 16 - 16 -	GAAG ThrG	G 15	GCCTG ::: hrVal	GAC Asp	rgG rgG	GCGT yVa	GACC	17 17	CAGC	A: A	er – 60	ACG 	SMe	Met	IACO	a - C
uAsp) L : 0	14 -	GTG uLy	GGCT	:ATCG ::: LeuG	GTAT	eeec	TCC	TCC 1eF	CAP AAs	PT-CCC	TGC ::	CAAA ::::: lyGl	t : .	TCA ::: Ala	0	: : :SMe
Gln	7 - 0	AG1 tva	TGAA sGlu	To	AGGC ::	CTAC eTyr	Arg	TGG.	Va Va	AGCC ::: pThr	± G	ATGA ::	GCAA :::: uArg	GA,	TGG - Jeu <u>A</u>	STh	ACAAG tLeuV
PheA	PT	CAG Arg	TT]	AA:	CTT	GAG GLu	ATTG ::: LeuA	AGCT	GAAG ::: Ser	CCCA : ProA	± :: ₹	GAA : gAs	CAC :::: Tyr	PTCT	CCCC snPr	AGGA rGly	1G 11 11
:: SpHi	GTCT	GTC Val	TCC::	Se :: G	CACC:::III	ACCC ::: Alap	ACAT	CTTC uVal	GTG :::	AACAC::: AspGl	AGC : uPr	CCTC ::: nIle	GGGA		CCAG :::	AAGG Lysg	AAA Lua
sLys	Ile CTC	TCCG:	pA1	TGAG ::::	ATGG ::: GlnT	CAGC	CGTG : :tVal	ATG Glu	CCA :::	uPr 	CCI	TCATGC:::::: ::::::::::::::::::::::::::::::	TTC :: alg	: 8	ღ:: ₽	GGAA YAS	CGC aAl
A G	YI A	TCCT::	₩ Q	CTGG : LeuI	ACC hrA		GAGA Glua	TACCT	ACGT :: :Lyva	TGAC	CCAG	CACATC	CCATC	· 0	AAAGG Lysv	CGA nAs	CCAC ::::
laG	CAATGAG ::: CAspala	CAAG : leLys	ATCG :	TGTAT :: leTyr	GGGAAG ::: laaspv	AGGCACCATO :: hLeuLeuVa	ACC snA	TGAAC euAsn	CAAG Met	CATTC::	GTCT :: :luIL	CAGCT gSerI	Pro III	AGG S	TCAT	TCAG pGln	CGGG ::: LysT
ne1 -	GAC G1u	GGCC :	CCAA :: 'ally	P A	ТС a 1		GCTT rgVa	GIU GIU	GG LeuA	TCGA::::	CTA : eTy	le AC	GTCAC	GCCG :: erAr	TGCT:	GTCC	GAGGG TyrG1
HIII YPhe	CTGG : LeuA	AGGT ::::: \snAl	GTC ::	GGGT gGly	ThrH	CTTTA	CATT	GTCG ::: :IleA	ATG spP	GA1	CACG rLeu	GAGG GLuA	IS	GAAI ::: gGlu	.p − 0	GGI rgP	GGC YA1
ATC	1G	GT/ ; aAs	CCAG:	TTAC Leu1	AAAAT Histy	ACCAT	GGA G1y	CGG aG	CAC ::	CGAG eGly	AAGA MetT	CTGG ag1	CCAAG ::: ysSer	AATGACCTG/ :::::: ::uGluThr]	laA	TTGA	CAAG aAsp
AACAT	AGCATG ::: ThrTyr	CATC ::: ;nVal	GAGC	rpTy	CAAA rLys	rgcrc pAlaH	ATGAA ::: IleLy	GCAA :: YAs	CACC : !Thr	TTC	ACCCA	AAT yPr	AAC ::: Ser	CTGA : !hr!		GCTC:::	AAGTATG AspAlav
TC 1 Le 3	'GA 1	CT 1	rg 	rs -	CA :: As	CAT His	AAGT Lyss	GCA : nHi	CAC	AAAA ::: GluL	AGGA :: /SA1	CCIG OLeu	CCGT	ATGGA	.TGG uTrp	AGCI SerI	FIGIC
182	.132	1082	1032 336	982 320	932 303	882 286	832 270	782 253	732 241	685 226	635 209	585 192	535 176	159	150	139	34 1 11

1183 AATTCCCTCAGGCTGAAG 1200

```
SSER BERRE SOCIOCIO COCOCERTA RESERVA DE RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: SwissProt_39:ASSY_ARCFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     387 TrpGlyLeuProThrLys 392
                                                                                                                                                                                                      alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                US-09-775-693-1 x ASSY_ARCFU
                                                                                                                                                                                                                                                                             percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASSY_ARCFU
                                                                                                 Align seg 1/1 to: ASSY_ARCFU from: 1 to: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., white O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Ketchum K.A., Dodson R.J., Graham D.E., Kyrpides N.C.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.G.,
Richardson D.L., Kerlavage A.R., Graham D.E., Sutton G.G., Gill S.
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:364-370(1997).
-i- CATALYTIC ACTIVITY: ATP + L-CITRULL.
-i- PYROPHOSPHATE + L-ARGININOSUCCINATE
PYROPHOSPHATE + L-ARGININOSUCCINATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWABL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute as long as its content is in no way use by non-profit institutions as long as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pfam; Pr00764; Arginosuc_synth; 1.
probom; PD003544; Arginosuc_synth; 1.
prosite; PS00564; ARGININOSUCCIN_SYN_1; 1.
pROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
pROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
complete proteome.
Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.
SEQUENCE 390 AA; 44104 MW; 31334D84F696EEBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000949; AAB89005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: PENULTIMATE STEP IN ARGININE BIOSYNTHESIS.
SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                 19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / DSM_4304 / ATCC 49558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                            750.50
2.544
72.482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP + L-CITRULLINE + L-ASPARTATE = AMP
                                                                                                                                                                                                                                                                                                percent Identity: 43.735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  390 AA.
                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhou L.,
```

```
113 TTGGCCAGAAGGAA...GACTTCGAGGAAGCCAGGAAGAAGGCACTGAAG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 GCTGAAGGAACAA...GGCTATGAC...GTCATTGCCTATCTGGCCAACA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 uLeuLysGluLysTyrGlyPheAspGluVallleThrValThrValAspI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 ACCTCCTGGGCACCTCTTGCCAGGCCCTGGATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 leGlyGlnProGluAlaAspIleLysGlnAlaGluGluArgGlyLysLys 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 GluvalalaLystysGluGiyalaGluAlaValAlaHisGlyCysThrGl 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 GAAATCGCCCAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 Tyr...AlaAspLysHisTyrThrIleAspAlaLysLysGluPhevalAs 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ValValLeuSerTyrSerGlyGlyLeuAspThrThrValCysIleProLe 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 pSer...LeuPheMetLeuTleLysAlaAsnGlyAsnTyrGluGly...T 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 CCCAG.....ATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTAC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 yLysGlyAsnAspGinLeuArgPheGlu......AsnIlePheA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 yrValLeuGlyThrAlaLeuAlaArgProLeuIleAlaGluLysValVal 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            504 GATTCCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACC 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                454 AACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 rgGlnH1sGlyPheLysValileAlaProValArgGluLeuAsnLeuThr 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 yIleGluValProAlaThrLysGluLysProTyrSerfleAspGluAsnL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604 GCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGGCCAAAGCCCCCCAA 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 euTrpSerArgSerValGluGlyGlyLysLeuGluAspProSerPheGlu 190
                                                                                                                                                                                                                                                                                                                                                                  654 CACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGG 703
                                                                                                                                                                                                                                                                                                                                                                                                                                           191 ProProGluAspileTyrGluTrpThrAlaSerProGluLysAlaProAs 207
                                                                                                                                                                                                                     754 ATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACAT 803
                                                                                                                                                                                                                                                                                            224 euAsnAspGluArgMetGly.......GlyPheGluLeuIle 235
                                                                                                                                                                                                                                                                                                                                704 TGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTC 753
                                                                                                                                                                                 804 CGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCC 853
                                                                                                          854 CAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACC 903
                                                                                                                                           252 tīleGluAspārgValLeuGlyLeuLysālaārgGluAsnTyrGluHisP 269
                                    904 ATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGC 953
                                                                        269 roAlaAlaThrIleLeuIleThrAlaHisArgAspLeuGluAsnLeuVal 285
286 LeuSerArgGluLeuLysPheLysLysPheValGluGluGluTrpAl 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAA 603
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: SwissProt_39:ASSY_METJA
                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Pfam; PF00764; Arginosuc_synth; 1.
                                                  interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                            EMBL; U67494; AAB98414.1; -. TIGR; MJ0429; -.
                                                                                                                                                                                                                                                                                            -1- PATHWAY: PENULTIMATE STED IN ARGININE BIOSYNTHESIS.
-1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                         Science 273:1058-1073(1996).
-(- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP + PYROPHOSPHATE + L-ARGININOSUCCINATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1195 CTGAAGGAATATCATCGTCTC 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1154 CAACTGAT......GCCACCGGGTTCATCAACATCAATTCCCTCAGG 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARGG OR MJ0429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1104 TCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGC 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q60174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 GlyArgLeuPheArgArgLeu 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASSY_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1054 TCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTC 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 erileAspGlnArgLeuAlaGluGLyPheAlaAlaPheHisGlyLeuGln 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1004 GCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAGGTG 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 aLeuTyrSerGluGluLeuValSerPhe......AspThrGluS 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 LysLeuTyrLysGlySerAlaValValValAlaArgAsnSerProTyrAl 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 snAlaPherieAspLysThrGlnGluArgValThrGlyTrpValLysVal 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 aGluLeuvalfyrTyrGlyLeuvalAsnAspProLeuPheAspAlaLeuA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         954 TGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCC 1003
                          IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 395 AA.
```

```
alignment_block:
US-09-775-693-1 x ASSY_METJA
214 eValGluIleGluPheLysGluGlyValProValAlaIleAsnGlyGluL 231
                        666 TCTCGAGATCGAGATTCAAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCA 715
                                                                               199 ileTyrAlaTrpThrLysAsnProValGlu...AspLysGluGluGluIi 214
                                                                                                                         616 CTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCTGACAT 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: ASSY_METJA from: 1 to: 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                              182 errleGluGlySerGluLeuGluAsnProAspPheValProProGluGlu 198
                                                                                                                                                                                      566 GCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCGCCTCCAGGT 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 747.00
Ratio: 2.630
Percent Similarity: 70.647
                                                                                                                                                                                                                                           166 o...ThrGluSerLysLysTyrSerIleAspGluAsnLeuTrpGlyArgS 182
                                                                                                                                                                                                                                                                                   516 GGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCA 565
                                                                                                                                                                                                                                                                                                                          150 ThrargalaGluGluIleGluTyralaLysGluLysGlyIleProllePr 166
                                                                                                                                                                                                                                                                                                                                                                466 GGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCATCCC 515
                                                                                                                                                                                                                                                                                                                                                                                                   138 euLysIleIleAlaProIleArg.....AspLeuAsnLeu 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                 416 TAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 yAsnAspGlnPheArgPheGluThrThrIleArgIleLysAlaProHisL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 GAACGATCAGGTCCGGTTTGAGGTCAGCTGCTACTCACTGGCCCCCCAGA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 AlaGluGluValGlyAlaGluAlaValAlaHisGlyCysThrGlyLysGl 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 GCCCAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 TGGGCACCTCTTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 CATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACCTCC 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 euSerThrAlaLeuAlaArgProLeuTleAlaHisLysValValGluTle 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 GCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGAGTT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 riiePheArgálaileLysAlaAsnálaMetTyrGluGly...TyrProL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 AG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 ValLeuLysHisTyrThrIleAspAlaLysGluGluPheValLysAspTy 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 inProGluGluGluIleLysGluValGluGluLysAlaLysLysLeuGly 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 uGluAspLysTyrGlyTyrLysValValSerValCysValAspValGlyG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 GAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTGGCC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 GTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTGGCT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN 1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.
SEQUENCE 395 AA; 44723 MW; 655D4A7AC06E7A7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 ValLeuAlaTyrSerGlyGlyLeuAspThrSerCysCysLeuLysLeuLe 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 43.035
```

1166 CCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATATCATCGTCTC :: ::::: :: :::::: 375 laGlyMetVal	1116 GGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATGCCA : : : : : : : : : : : : : : : : : :	1066 GGCCAGGTGTACATCCTCGGCCGGGAGTCCCCCACTGTCTCTACAATGA ::: ::::: ::: :::	1016 CCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAGGTGTCCGTCC	966 TACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCATCG	916 GTGCGCAAAATCAAACAAGGCCTGGGGTTGAAATTTGCTGAGCTGGTGTA :::::: ::: ::::: ::: 293 GluLeuArgPheLysGluIleValAspSerLeuTyrGlyGluLeuIleTy	866 TCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGATGAACCATGAACCATGAACCATGAACCATGAACCATGAACCATGAACCATGAACCATGAACAACAACAACAACAACAACAACAACAACAACAACAAC	816 CTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCACCA ::: :::	766 GAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAACCG :::	716 AGGATGGCACCACCAGCAGACCTCCTTGGAGCTCTTCATGTACCTGAAC
3AAGGAATATCATCGTCTC ::: LysTyrHisGlyLeu	PATGAGCCAACTGATGCCA::::::::::::::::::::::	ACTGTCTCTACAATGA ::: ::::: OTyrAlaLeuTyrSerLy	CAGGTGTCCGTCCTCAAG ::: :::::::: LysValLysLeuPheGly	TTGTCCGCCACTGCATCG::: spleuAspAlaPheIleA	ATTTGCTGAGCTGGTGTA ::::: ::: uTyrGlyGluLeuIleTy	TTCACCATGGACCGGGAA::::::::::::::::::::::	AGACCCCAGCAGGCACCA ::::::::: uCysProGlyAlaValL	TGACATCGTGGAGAACCG ::: eAspIleIleGluAspAr	
1 283		359	1065	1015	309	915 292	865 276	815 259	765 242

, ,			
••			
ĺ			
1			
ř			
Ì			
Ţ [*]			
•			

Date: Feb 12, 2002 4:10 PM

Command line parameters:

gearch information block:
 Query: US-09-775-693-1
 Query length: 1239
 Database: SPTREMBL_17:*

```
OM of: US-09-775-693-1 to: SPTREMBL_17:* out_format: pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database: SPTREMBL_17:*
Database sequences: 473505
Database length: 146272329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search time (sec): 125.310000
                                                                                                                              sp_invertebrate:Q9BKV7 +
sp_vertebrate:057591 + 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strd Orig
                                                                                                                                                                                                                                                                                                                                                                                                                                                   rd Orig 2Score 1234.00 1216.81 1034.00 1216.81 115.84 1948.50 1049.24 1892.00 1049.24 1892.00 1049.24 1815.00 956.64 1815.00 956.64 1815.00 894.83 56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.56 1751.50 883.50 883.56 1751.50 883.50 883.50 883.50 883.50 883.50 883.50 883.50 883.50 883.50 883.50 883.50 883.50 883.50 883.50 883.50 883.50
                                                                   149.00 1
148.50 1
146.00 1
142.00 1
142.00 1
                                                                                                                                                                                                                                                                                                                                                          298.
251.
                                                                                                                                                                                       156.50
155.50
153.00
                                                                                          194.45
174.72
172.76
166.71
                                                                                                                                                                                                  175.02
179.69
                               160.16
153.49
165.77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESCOTE Len

9.4e-73 40

4.2e-60 40

1.7e-54 40
                                                                                                                                                                              .30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.3e-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.7e-43
3.6e-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.9e-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.5e-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1e-53
                                                                                                                                                                                                                                                             1.3e-19
2.1e-19
1.3e-16
2.6e-16
2.6e-12
9.7e-09
0.0004
0.0034
0.0037
0.0126
0.0126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.0e-45
0.0604
0.0871
0.1623
0.1771
0.2371
0.2155
0.2335
0.2555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5e-41
                                                                                                                                                            0.0434
                                                                                                                                                                                                                                           0.0191
                                                                                                                                                                                                  0.0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .3e-27
.3e-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ! Documentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9xvi4 thermotoga maritima. arg Q9xvi4 deinococcus radiodurans. Q9rwi4 deinococcus radiodurans. Q9rwi4 deinococcus rescentus. Q9abul caulobacter crescentus. Q9pkt campylobacter jejuni. arg Q9k820 bacillus halodurans. arg Q9k820 bacillus halodurans. arg Q9k820 bacillus halodurans. arg Q9k820 bacillus halodurans. arg Q9k823 arabidopsis thaliana (mg Q9szx3 arabidopsis thaliana argi Q9ky4z3 moritella sp. 2693. argi Q9yc7 staphylococcus aureus su Q9ynt8 vibrio cholerae. arginin Q9hnt8 vibrio cholerae. arginin
                                                                                   1 057591 fugu rubripes (japanese p
1 09ntq6 homo sapiens (human). hy
1 09m715 zea mays (malze). arabin
1 09m701 deinococcus radiodurans
1 09rv01 deinococcus radiodurans
1 09rv01 homo sapiens (human). ki
                                                                                                                                                                                                                                                                                                                                                      Q9jwml neisseria meningitidis (Q9jwml neisseria meningitidis (Q9fc47 streptomyces coelicolor Q9fc47 streptomyces coelicolor Q9pem9 xylella fastidiosa. argi Q9v2z3 methanobacterium thermoa Q9v2z3 methanobacteriums hydroge Q9f8m0 carboxydothermus hydroge Q9khb9 erwinia chrysanthemi. ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                029262 sus scrofa (pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Q99621 homo sapiens (human)
1 Q9ctw8 mus musculus (mouse)
1 Q68872 myxococcus xanthus. hy
1 Q99495 homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V23707 sus scrofa (pig). arginin
Q9jxc1 neisseria meningitidis (
                                                                                                                                                                                                                                                                                           Q945k9 herpesvirus papio. ntr
Q9uIB3 homo sapiens (human). hy
Q9sdm2 triticum aestivum (wheat
                                                                                                                                                                                                                                                       004210 arabidopsis thaliana (1
                                                                                                                                                                                         Q9ufs5 homo sapiens (human).
1 Q9bkv7 leishmania major. F
                                                                                                                                                                                                                                  Q9sdm3 triticum aestivum (wheat
                                                                                                                                                                                                                ppg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_human:09U039
sp_human:09U040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_rodent:Q62105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_human:Q9UHA8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_virus:Q9DWH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: sp_bacteria:Q9X2A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                            percent similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99287316; PubMed-10360571;
MEDLINE-99287316; PubMed-10360571;
Nelson K.E., Clayton R.A., Gill S.R., Nelson M.C., Ketchum K.A.,
Haft D.H., Hickey E.K., Peterson J.D., Linher K.D., Garrett M.M.,
McDonald L., Utterback T.R., Malek J.A., Fhillips C.A., Richardson D.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., White O.,
Stewart A.M., Cotton M.D., Venter J.C., Fraser C.M.;
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Stewart A.M., Cotton M.D., Venter J.C., Fraser C.M.;
Beidelberg J., Smith H.O., Venter J.C., Fraser C.M.;
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                               US-09-775-693-1 x Q9X2A1
                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: Q9x2Al from: 1 to: 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prolom; Prou/04; Arginosuc_synth; 1.

ProDom; PD003544; Arginosuc_synth; 1.

PROSITE; PS00564; ARGININOSUCCIN_SYN_2; 1.

PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.

ATP-binding; Arginine biosynthesis; Complete proteome; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001518; Arginosuc_synth.
                                                                                                 110 ACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAG 159
                                                                                                                                                                                                                         PATHWAY.

PATHWAY: HOMOTETRAMER (BY SIMILARITY).

SUBJUST: HOMOTETRAMER (BY SIMILARITY: TO THE ARGININOSUCCINATE SYNTHASE FAMILY SIMILARITY: ABOOL816; AAD36844.1; ...
                                                                                                                                                                              60 CCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCA 109
                                                                                                                                          18 eLeuLysTrpLeuCysGluLysGlyPheAspValileAlaTyrValAlaA 35
                                                               35 snvalGlyGlnLysAspAspPheValAlaTleLysGluLysAlaLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermotogales; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 1226.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 AA; 46054 MW; ECCDC8575E962482 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139.50
139.00
139.00
139.00
139.00
                                                                                                                                                                                                                                                                                                                                                                                                                          3.683
82.222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164.27
157.27
153.63
151.21
146.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 percent Identity: 59.012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.2353
0.2763
0.2900
0.2995
0.3209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
629
956
1262
1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Q62105 mus musculus (mouse).
| Q9dwh3 rat cytomegalovirus (
| Q9uq39 homo sapiens (human).
| Q9uq30 homo sapiens (human)
| Q9uq40 homo sapiens (human)
```

sp_bacteria:09ABUl sp_bacteria:Q9RWJ4 sp_bacteria:Q9x2A1

sp_bacteria:Q9K4Z3 sp_bacteria:Q9K820 sp_bacteria:Q9PHK7

sp_bacteria:09K4Y8 sp_plant:Q9SZX3

sp_archea:Q9UX31 sp_human:O43348 sp_bacteria:Q9KNT8

sp_archea:Q9HMQ2

sp_bacteria:Q9JWM1 sp_bacteria:Q9FC47

sp_bacteria:09PEM9 sp_bacteria:09JXC1

sp_bacteria:Q9F8M0 sp_bacteria:Q9KHB9 sp_archea:Q9V2Z3

sp_plant:Q9SDM2 sp_human:Q9C0J8 sp_virus:0905K9

sp_human:Q9UF83

sp_plant:09SDM3 sp_plant:004210

sp_human:Q9UFS5

sp_bacteria:Q9RV01 sp_human:Q94850 sp_human:Q99621

sp_human:Q99495 sp_rodent:Q9CTW8 sp_human:Q9NTQ6 sp_plant:Q9M7I5

```
1060 CTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTA 1109
                                              1010 GCATCGCCAAGTCCCCAGGAGCGAAGTGGAAAGTGCAGGTGTCCGTC 1059
                          335 laPheArgLysAlaGinGluAsnValThrGlyLysValThrValSerIle 351
                                                                                       318 uIleTyrAsnGlyPheTrpPheSerProGluMetGluPheLeuLeuAlaA 335
                                                                                                       960 GGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACT 1009
                                                                                                                                                302 LysGluValMetHisLeuArgAspMetLeuAlaProLysPheAlaGluLe 318
                                                                                                                                                                              910 CGGGAAGTGCGCAAAATCAAACAAGGCCTGGGGCTTGAAATTTGCTGAGCT 959
                                                                                                                                                                                                          285 laThrIleLeuTrpIleAlaHisArgAspLeuGluGlyIleThrMetAsp 301
                                                                                                                                                                                                                                     860 GCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGAC 909
                                                                                                                                                                                                                                                                  268 uAsnArgPherleGiyrleLysSerArgGiyValTyrGluThrProGlyA 285
                                                                                                                                                                                                                                                                                              810 GAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAG 859
                                                                                                                                                                                                                                                                                                                           252 LeuAsnGluValGlyAlaLysAsnGlyValGlyArgLeuAspMetValGl 268
                                                                                                                                                                                                                                                                                                                                                 760 CTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCCGTATTGACATCGTGGA 809
                                                                                                                                                                                                                                                                                                                                                                                     235 snieulysaspGlyThrGluLysThrAspProLeuGluLeuPheGluTyr 251
                                                                                                                                                                                                                                                                                                                                                                                                                    710 ACGTCAAGGATGGCACCCACCCACCAGGCCTCCTTGGAGCTCTTCATGTAC 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                218 uThrLeuLeuGluileHisbheGluAsnGlyIleProValLysValValA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    660 TGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTTGTGAAGGTGACCA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 GluAspValPheThrTrpThrValSerProLysAspAlaProAspGluGl 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       610 CCAGGTCTCTACACGAAGACCCAGGCCAAGCCCAAAGCCCCCAACACCCCC 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 isileSerHisGluAlaGlyLysLeuGluAspProAlaHisIleProAsp 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                560 ACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 oIleLysValSerLysLysArgProTyrSerGluAspGluAsnLeuWetH 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         510 CATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 PheLysGlyArgThrAspLeuIleAsnTyrAlaMetGluLysGlyIlePr 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 roAsnLeuLysValileSerProTrpLysAspProGluPheLeuAlaLys 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   410 CCGAGATAAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 yLysGlyAsnAspGlnValArgPheGluLeuThrTyrAlaAlaLeuAsnp 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 GluileAlaGluLysGluGlyAlaGlnTyrvalAlaHisGlyAlaThrGl 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 GAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCCACGGCGCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 ACCTCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 yrLeuLeuGlyThrAlaIleAlaArgProLeuIleAlaLysArgGlnVal 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 rAspTyrilePheThrAlaLeuLeuGlyAsnAlaMetTyrGluGlyArgT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 ThrGlyAlaSerLysValTyrValGluAspLeuArgArgGluPheValTh 68
```

```
alignment_block:
US-09-775-693-1 x Q9RWJ4
                                                                                                                                                                                                                    alignment_scores:
                                                              Align seg 1/1 to: Q9RWJ4 from: 1 to: 402
                                                                                                                                                      Quality: 1034.00
Ratio: 3.272
Percent Similarity: 76.886
                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID Q9RWJ4 PRELIMINARY;
7 AGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGGCCTGGACACCTCGTG 56
                                                                                                                                                                                                                                                                                          InterPro; IPR001518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; I;
ProDom; PD003544; Arginosuc_synth; I;
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: sp_bacteria:Q9RWJ4
                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                 ATP-binding; Arginine biosynthesis; Complete proteome; Ligase;
                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: TO THE ARGININOSUCCINATE SYNTHASE FAMILY. TIGR: DR0674; - AAF10250.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1 ", 25clence 286:1571-1577(1999).

Science 286:1571-1577(1999).

-i- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE ~ AMP + PARTHAAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC DATHMAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White O., Elsen J.A., Heidelberg J.F., Hickey B.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Weisen H., Jiang L., Pamphile W., Crosby M., Shen M., Watarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Eraser C.M.; Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O9RWJ4;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1210 CGTCTCCAGAGCAAG 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1160 ATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATATCAT 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 GlnLeuValLysLys 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1110 CAATGAGGAGCTGGTGAACGTGCAGGGTGATTATGAGCCAACTG 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 spSerLysGlyPheileAsnileHisAlaLeuArgLeuLys...ValHis 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 rAsnProGluLeuSerSerMetAspValGluGlyGlyPheAspAlaThrA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 TyrLysClyAsnValMetProValAlaArgTyrSerProTyrSerLeuTy 368
                                                                                                                                                                                                                                         402 AA; 44877 MW; 8694AD1424A99835 CRC64;
                                                                                                                                           Percent Identity: 50.122
```

```
204 TGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 CTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 TGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454 AACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              404 TGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTAC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 aThrGlyLysGlyAsnAspGlnValArgPheGluMetSerAlaTyrAlaL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 CACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCAC 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 CAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 ACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 yIleProValProThrThrLysLysAspProTrpSerMetAspAlaAsnM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 CATCCTCGTGTGGCTGAAG...GAACAAGGCTATGACGTCATTGCCTATC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 LeuAsnThrGlyAlaValAlaAlaTyrAlaLeuAspLeuArgGluGluPh 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 \hspace{0.1cm} \textbf{eIleLeuLysTrpLeuGlnThrGluArgAsnTyrAspValValCysPheT} \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        654 CACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGG 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 ProProThrHisMetPheLysLeuThrValAsnProGluAspAlaProSe 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 lyTyrTyrLeuLeuGlyThrSerIleAlaArgProLeuIleAlaLysLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 eValArgAspTyrValPheProMetMetArgSerSerAlaLeuTyrGluG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 hrAlaAspLeuGlyGlnGlyAspGluValGluGluAlaArgValLysAla
                                                                                                                                                                                                                                                                                                                                                           243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                        904 ATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGC 953
293 LeuAspArgGluValLeuHisGlnArgAspAlaLeuGlyProLysTyrAl 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt SerLysGluLysIleValLeuAlaTyrSerGlyGlyLeuAspThrSerIl~18}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      etLeuHisIleSerTyrGluGlyGlyProLeuGluAspProTrpThrGlu 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACC 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAA 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     euLysProAspIleValThrValAlaProTrpArgAspTrpAsp..... 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ......PheGlnGlyArgAlaAspLeuGluAlaPheAlaArgGluHisGl 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTC 753
                                                                                                                                                                          CAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACC 903
                                                                                                                                                                                                                                          CGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCC 853
                                                                                                                                                                                                                                                                                                                                                        ThrLysAlaAsnGluIleAlaGlyArgHisGlyValGlyArgIleAspLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leAsnGly.....GluGlnLeuSerProAlaAlaLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roGlyGlyThrLeuLeuTyrHisAlaArgArgAlaValGluSerLeuThr 292
                                                                                                                                                                                                                                                                                                                                                                                                                    ATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACAT 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :: :
                                                                                                                                                                                                                                                                                                                                                                        259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242
```

```
seq_name: sp_bacteria:Q9ABU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                            alignment_block:
US-09-775-693-1 x Q9ABU1
                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                Align seg 1/1 to: Q9ABU1 from: 1 to: 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1042 AAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGA 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1142 GTGATTATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTC 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1092 GTCCCCACTGTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGG 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1192 AGGCTGAAGGAATATCATCGTCTCCAGAGCAAG 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 lnValTyrPheAspHis...ValAlaLysSer.....ValThrGly 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21173698; PubMed=11259647;
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Risen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
DeBoy R.T., Dodson R.J., Durkin A.S., Khouri H., Shetty J., Berry K.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Kolonay J.F., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 sAlaGluArgSerLeuTyrAspLysAspLeuValSerPheGluAlaGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 ThrAlaArgLeuLysLeuTyrLysGlyAsnCysIleValAlaGlyArgLy 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                954 TGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAA...... 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 lyAspTyrAsnGlnHisAspAlaGlyAlaPheIleLysLeuAsnSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389 ArgMetArgValGlnLysArgValGluAspLys 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC0129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARGININOSUCCINATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9ABU1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 408 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR; CC0129; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=69394;
                69 GCTGAAG...GAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                 19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG
                                                          9 ValValLeuAlaTyrSerGlyGlyLeuAspThrSerIleIleLeuLysTr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....TTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGG 1041
                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                             948.50
3.090
76.559
=
                                                                                                                                                                                                                                                                                                                                                                                                 45330 MW;
                                                                                                                                                                                                                                          eaps: 8
Percent Identity: 50.125
:::||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                   06571CBDC38B0FBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408 AA
```

```
316 aSerLeuValTyrAsnGlyPheTrpPheSerProGluArgGluMetLeuG
                                                    954 TGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCC 1003
                                                                                                                                                                904 ATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGC 953
                                                                                                                                                                                                                                                                             854 CAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACC 903
                                                                                                                                                                                                                                                                                                                                                                  804 CGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCC
                                                                                                                                                                                                                                                                                                                                       250 ThrLysLeuAsnGluLeuGlyArgAspAsnGlyValGlyArgLeuAspLe 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     754 ATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGGCCGTATTGACAT 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              654 CACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  704 TGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTC 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       604 GCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAA 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 nIleThrLysAspLysArgGlyGluAlaProPheSerValAspAlaAsnL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                510 CATCCCGGTCACTCCCAAGAAC.....CCGTGGAGCATGGATGAGAACC 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 PheLysSerArgGluAlaLeuLeuAspPheAlaGluLysHisGlnIleGl 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 yLysGlyAsnAspGlnValArgPheGluLeuGlyTyrTyrGlyLeuGluP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 GAAATCGCCCAGCGGAGGGGGGCCAAGTATGTGTCCCACGGCGCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 ACCTCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 GCCAAA.....AAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 yrLeuLeuGlyThrSerIleAlaArgProLeuIleAlaLysLysGlnIle 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 gAspTyrValPheProMetPheArgAlaAsnThrValTyrGluGlyGlnT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 ValLysProGluAsnIlePheIleGluAspValArgGluGluPheValAr 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42
                                                                                                            LeuAspArgGlyAlaMetHisLeuLysAspGluLeuMetProLysTyrAl 316
                                                                                                                                                                                                                           {\tt roGlyGlyThrIleLeuLeuAlaAlaHisArgGlyIleGluSerIleThr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                le.....AspGlyValAla...MetSerProAlaThrLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pAlaProThrIleIleThrIleAspPheGluLysGlyAspProValAlaI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt AlaProGluPheValHisMetArgThrIleAlaProGluAspAlaProAs}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euLeuHisSerSerGluGlyLysValLeuGluAspProAlaValGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt GluIleAlaArgLysMetGlyAlaAspAlaValSerHisGlyAlaThrGl}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt lyGlnGlyGluGluIleGluProAlaArgAlaLysAlaLeuAlaAlaGly}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pLeuGlnThrGluTyrGlyAlaGluValIleThrPheThrAlaAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249
```

```
Seq_documentation_block:
ID Q9HY84
AC Q9HY84
DT 01-MAR-2001 (TrEMBLre DF 2001 (TREMBLR
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: sp_bacteria:Q9HY84
                                                                                                                                                                                                                           Pfam; PF00764; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20437337; PubMed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V., "Omplete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Nature 406:959-964(2000)
-i- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP + PYROPHOSPHATE + L-ARGININGSUCCIARTE.
                                                                                                                                                                                                                                                                                                                                                                                           PATHWAY.

1: SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

1: SIMILARITY: TO THE ARGININGSUCCINATE SYNTHASE FAMILY EMBL; AE004773; AAG06913.1; -
                                                                                                                                                                    ATP-binding; Arginine biosynthesis; Complete proteome; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1148 ATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1198 AAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1104 TCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGAT.....T 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1054 TCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTC 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1004 GCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGGAAAGTGCAGGTG 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 yrAspHisArgAspAlaGlyGlyPheIleLysLeuAsnAlaLeuArgLeu 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 rLeuTyrAspClnAspLeuValThrPheGlu...GluGlyLysValAlaT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399 Arg 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 LysLeuTyrLysGlyAsnValThrValIleGlyArgGluSerProTyrSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 lnAlaAlaIleAspTyrSerGlnAspLysValThrGlyArgValArgVal
                                                                                                         405 AA; 45297 MW; 1C3DB39EB18689E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366
```

alignment_block:

US-09-775-693-1 x Q9HY84

Percent Similarity:

927.50 3.011 76.238

Percent Identity: 47.030

Length:

Quality: Ratio:

ʹ

ر ہ

```
Align seg 1/1 to: Q9HY84 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 CGCAAACAAGTGGAAATCGCCCAGCGGGGGGGGGCCAAGTATGTGTCCCA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 ATGAGGACCGCTACCTCCTGGGCACCTCTTGCCAGGCCCTGCATCGCC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 yrGluGlyGluTyrLeuLeuGlyThrSerIleAlaArgProLeuIleAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCGTGCATCCTCGTGTGGCTGAAGGAA...CAAGGCTATGACGTCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetAlaAspValLysLysValValLeuAlaTyrSerGlyGlyLeuAspTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uGluPheValArgAspPheValTyrProMetPheArgAlaAsnThrValT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGGCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hrPheThrAlaAspLeuGlyGlnGlyGluGluValGluProAlaArgAla 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt rSerValIleLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalTalTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValTalLeuLysTrpLeuGlnAspThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValTalLeuLysThrTyrAsnCysGluValLeuLysThrTyrAsnCysGluValLeuLysThrTyrAsnCysGluValLeuLysThrTyrAsnCysGluValLeuLysThrTyrAsnCysGluValLeuLysThrTyrAsnCysGluValLeuLysTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACACGGGATTCCCATCCCG.....GTCACTCCCAAGAACCCCGTGGAGCA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGTTTGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysAlaArgAlaMetGlyValLysGluIleTyrIleAspAspLeuArgGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuLeuSerArgGluLys.....LeuMetAspTyrAlaGluLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yrAlaLeuLysProGlyValLysValIleAlaProTrpArgGluTrpAsp 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGCGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAAGCCCCCAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGG 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrTrpThrGluHisGluGluAspMetTrpLysTrpThrAlaSerProGl 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCAAGAACCAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sHisGlyIleProIleGluArgHisGlyLysLysLysSerProTyrSerM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTCACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAA 447
TCTACGAGACCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATC
                                                                                         CCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGÍA 841
                                                                                                                                                                                                                                                                                                AlaGluValLeuThrGluLeuAsnArgValGlyGlyIleAsnGlyIleGl 258
                                                                                                                                                                                                                                                                                                                                                                                               TTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGG 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spIleValAlaIle......AspGly...LysAspMetThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uAsnAlaProAspThrProThrTyrIleGluLeuThrTyrArgLysGlyA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
          891
```

```
seq_documentation_block:
ID Q9PHK7 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: sp_bacteria:Q9PHK7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1042 AAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGA 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1189 CTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1092 GTCCCCACTGTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
argininosuccinate synthase (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9PHK7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 sSerAspAspSerLeuPheAspAlaAsnIleAlaThrPheGluGluAspG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325 rgLeuMetLeuGlnGlnMetIleAspAlaSerGlnValAsnValAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 GluSerIleThrLeuAspArgGluValAlaHisLeuLysAspGluLeuMe
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=NCTC 11168;
BTRAIN=NCTC 11168;
MEDLINE=20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.
Basham D., Chillingworth T., Moule S., Pallen M.J., Penn C.W.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
                                  Pfam; PF00764; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
ATP-binding; Arginine biosynthesis; Complete proteome; Ligase;
                                                                                                                                                                                                                                                                                                      reveals hypervariable sequences.";
Nature 403:665-668(2000).
-i- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; epsilon subdivision; Campylobacter
                                                                                                                                            -i- SIMILARITY: TO THE ARGININOSUCCINATE SYNTHASE FAMILY EMBL; AL139075; CAB75297.1; -. Interpro; IPRO01518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campylobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campylobacter jejuni.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARGG OR CJ0665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIGASE).
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       "The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=197;
                         Urea cycle.
                                                                                                                                                                                                                   - ! - SUBUNIT: HOMOTETRAMER (BY SIMILARITY)
                                                                                                                                                                                                                                                           -!- PATHWAY: UREA CYCLE, PENULTIMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValValArgLeuLysLeuTyrLysGlyAsnValValValValGlyArgLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTGAAATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGCCTTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ysTyrGluThrProGlyGlyThrIleMetLeuLysAlaHisArgAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tProLysTyrAlaSerLeuIleTyrThrGlyTyrTrpTrpSerProGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuArgMetArg 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGAT...TATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lyGlyAlaTyrAsnGlnAlaAspAlaAlaGlyPheIleLysLeuAsnAla
                                                                                                                                                                                                                                          PATHWAY.
                                                                                                                                                                                                                                                                                    PYROPHOSPHATE + L-ARGININOSUCCINATE
  406 AA;
  45578 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
  8A1E137AF30EC77F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               406 AA
                                                                                                                                                                                                                                                                      STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                group;
```

```
alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: Q9PHK7 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-775-693-1 x Q9PHK7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                  757 TACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGT 806
                                                                                                                                                                                                                                                                                                                                                                                                                            557 TGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCG 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 pIleSerLysLysLysGlyLysSerProTyrSerMetAspAlaAsnLeuL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 yLysGlyAsnAspGlnValArgPheGluLeuGlyTyrLeuAlaPheSerP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 GAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 ACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 GCCAAAAAG.....GTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 GCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 sAspTyrValPheProMetPheArgAlaAsnAlaIleTyrGluGlyGluT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 IleLysGluGluAsnIlePheIleLysAspLeuArgAspGluPheValLy 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 lyGlnGlyGluGluLeuGluProAlaArgLysLysAlaLeuSerLeuGly 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 pLeuGlnAspGluTyrAsnCysGluValValThrPheThrAlaAspIleG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 GCTGAAG...GAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       snGlyGluLys.....LeuSerProAlaGlyLeuLeuThr 248
                                                                                                                                                                      uSerGluIleIleGluLeuAspPheGlnLysGlyAspLeuValAlaIleA 237
                                                                                                                                                                                                                                                                          GluGluAspMetTrpArgTrpSerLysSerProLysAspAlaProAsnGl 220
                                                                                                                                                                                                                                                                                                                          CCTCCAGGTCTCTACACGAAGACCCCAGGACCCAGCCAAAGCCCCCCAACAC 656
                                                                                                                         CCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTCATG 756
                                                                                                                                                                                                                        CCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGGTCCCTGTGAAGGTGA 706
                                                                                                                                                                                                                                                                                                                                                                         euHisIleSerTyrGluGlyLeuValLeuGluAspProAlaHisAlaPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATCCCGGTCACTCCC...AAGAACCCGTGGAGCATGGATGAGAACCTCA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :::|||||| ::: ||||||
|GlnIleAlaLeuGlnThrGlyAlaAspAlaValSerHisGlyAlaThrGl 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            roAspLeuLysIleIleAlaProTrpArgGluTrpAspLeuAsnSerArg 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YrLeuLeuGlyThrSerIleAlaArgProLeuIleAlaLysThrGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG
       ====::::::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                892.00
3.014
74.559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuLeuAlaTyrAlaGlnLysHisGlyIleAs 170
oaps: 6
Percent Identity: 47.355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
```

```
seq_name: sp_bacteria:09K820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _documentation_block:
                               -!- SIMILARITY: TO THE ARGININOSUCCINATE SYNTHASE FAMILY EMBL; APO01518; BAB06906.1; -
InterPro; IPR001518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1154 CAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGG 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1104 TCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGC 1153
                                                                                                                                                                                                                                                  halodurans and genomic sequence comparison with Bacillus subtilis Nucleic Acids Res. 28:4317-4331(2000).
-i-CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP + PYROPHOSPHATE + L-ARGININOSUCCINATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1057 GTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTG...TC 1103
ATP-binding; Arginine biosynthesis; Complete proteome; Ligase; Urea cycle.
                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                       -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY)
                                                                                                                                                                                                                           -!- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus halodurans.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARGG OR BH3187.
                                                                                                                                                                                                                                                                                                                                                                    Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIGASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9K820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 laLeuIleAspGluSerGlnIleHisAlaAsnGlyArgValLysLeuGlu 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 LysLeuAsnGluLeuGlyCysLysHisGlyIleGlyArgLeuAspIleVa
                                                                                                                                                                                                                  PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lnLysAspAlaAlaGlyPheIleLysLeuAsnAlaLeuArg 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rLeuPheAsnAlaAlaTyrCysThrPheGluGluAspGluValTyrAsnG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuTyrLysGlyAsnValMetValIleGlyArgGluSerAlaAsnAspSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAGGTGTCC 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rLeuIleTyrAsnGlyTyrTrpPheSerProGluArgMetMetLeuGlnA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCC 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGA 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lyGlyThrIleLeuLeuLysAlaHisArgAlaLeuGluSerIleThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAG 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspArgGluAlaAlaHisLeuLysAspGluLeuMetProLysTyrAlaSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298
                                                                                                                                                                                                                                                                                                                 subtilis.";
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: Q9K820 from: 1 to: 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 865.00
Ratio: 2.912
Percent Similarity: 72.439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-775-693-1 x Q9K820
230 ..AsnGlyLysSerTyrProValHis.....GluLeuIleLeu 241
                                              707 CCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATG 756
                                                                                                                                               657 CCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGAAGGTGA 706
                                                                                                                                                                                              197 ProGluGlyAlaTyrGluLeuThrValAlaIleGluAspAlaProAspGl 213
                                                                                             213 nProGluIleValGluIleGlyPheGluLySGlyIleProValThrLeu. 229
                                                                                                                                                                                                                                                                                              180 rpGlyArgSerAsnGluCysGlyIleLeuGluAspProTrpAlaThrPro 196
                                                                                                                                                                                                                                                                                                                                             557 TGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCG 606
                                                                                                                                                                                                                                                                                                                                                                                            163 eProIleProIleAspLeuAspAsnProTyrSerValAspGlnAsnLeuT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                        507 TCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 .....SerArgAspGluGluIleGluTyrAlaLysLysAsnAsnIl 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         457 CGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGAT 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 snProAsnLeuGluValLeuAlaProValArgGluTrpAlaTrp...... 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         407 CCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAAC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 AGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTCACTGG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 ValGlurleAlaGluGlnThrGlyAlaGlnAlaValAlaHisGlyCysTh 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 GTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 GCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 GGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 CCAACATTGGCCAGAAGGAAGACTTCGAGGAAGGCAGGAAGAAGGCACTG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 ysTyrProLeuValSerAlaLeuSerArgProLeuIleSerLysLysLeu 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 LysValGlyAlaIleGluSerTyrThrIleAspAlaLysLysGluPheAl 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 euAspValGlyGluGlyLysAspLeuGluPheValLysGluLysAlaLeu 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 lAlaileLysTrpLeuSerAspLysGlyTyrAspVallleAlaValGlyL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 CATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTG 56
                                                                                                                                                                                                                                               CCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACAC 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rGlyLysGlyAsnAspGlnValArgPheGluValSerIleGlnAlaLeuA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aGluGluPheValLeuProAlaLeuGlnAlaHisAlaLeuTyrGluGlnL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45490 MW; 169ED574AD55D22A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 44.878
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: sp_bacteria:Q9K4Z3
        Xu Y., Liang Z., Legrain C., Ruger H.J., Glansdorff N.;
"Evolution of Arginine biosynthesis in the bacterial domain: Novel
gene-enzyme relationships from psychrophilic moritella strains
(vibrionaceae) and evolutionary significance of n-alpha-acetyl
ornithinase.";
InterPro; IPR001518; Arginosuc_synth
                                                                                         J. Bacteriol. 182:1609-1615(2000).

-!- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP + PYROPHOSPHATE + L-ASGININOSUCCINATE.

-!- PATHMAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1157 CTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATAT 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1107 CTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAA 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1207 CATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1057 GTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCCACTGTCTCT 1106
                                                                                                                                                                                                                                                                            MEDLINE-20158877; PubMed=10692366;
                                                                                                                                                                                                                                                                                                           STRAIN=2674
                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1007 ACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAGGTGTCC 1056
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ARGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392 SerMetValAsnLysGluMetLysGluLys 401
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=111291;
                                                                                                                                                                                                                                                                                                                                                                                                                       Moritella sp. 2674
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIGASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9K4Z3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9K4Z3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 snAlaAlaValGlyPheIleSerLeuTrpGlyLeuProThrLysValTyr 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 uTyrAsnGluLysLeuAlaThrTyrThrProAspAspGluPheAspHisA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 LeuPheLysGlyHisAlaIleValGluGlyArgLysSerGluTyrSerLe 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 laPheLeuLysGluThrGlnSerThrValThrGlyValValArgValLys 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 uLeuIleTyrGluGlyLeuTrpPheSerProLeuGlnProAlaLeuSerA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    957 GCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCC 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 ThrLysGluValAlaHisPheLysProValValGluLysLysIleAlaGl 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                907 GACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 lyAlaMetThrLeuIleLysAlaHisLysGluLeuGluAspLeuThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         857 CAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 lGluAsnArgLeuValGlyIleLysSerArgGluValTyrGluCysProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      807 GGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAG 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291
```

```
SQ KW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-775-693-1 x Q9K4Z3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: Q9K4Z3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proDom; PD003544; Arginosuc_synth; 1.
proStTE; pS00564; ARGININOSUCCIN_SYN_1; 1.
pROStTE; pS00565; ARGININOSUCCIN_SYN_2; 1.
pROSTTE; pS00565; ARGININOSUCCIN_SYN_2; 1.
ATP-binding; Arginine biosynthesis; Ligase; Urea cycle.
SEQUENCE 404 AA; 44291 MW; EBEBAFBAB4E87F20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00764; Arginosuc_synth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 ACATTGGCCAG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 GCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 GGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 AAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                             170 pIleProThrAlaAlaSerAlaThrLysIleTyrSerArgAspAlaAsnA 187
                                                                                                                                                                                                                                                                                                                                                               504 GATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACC 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454 AACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 lGluAsnTyrIleTyrProThrLeuLysThrGlyAlaValTyrGluGlyT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 GCTGAAGGAACAAGGCTATGAC.....GTCATTGCCTATCTGGCCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 ValValValAlaTyrSerGlyGlyLeuAspThrSerValIleLeuProTr 26
                                                                                                                                                                                                    187 laTrpHisIleSerHisGluGlyGlyGluLeuGluAspProTrpAsnGln
                                                                                                                                                                                                                                                        554 TCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCAAGAACCAA 603
                                                                                                                                                                                                                                                                                                                                                                                                                 156 .....LeuThrSerArgGluSerLeuLeuGluTyrLeuAlaGluArgAs 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  654 CACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGG 703
                                                                                                204 ProSerLysGlnValTrpThrMetThrValAspProIleAspAlaProAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaSerGlyAlaSerGluCysTyrValValAspLeuLysAspGluLeuVa 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spValGlyGinGlyAlaGluGluLeuGluGlyIleGluAlaLysAlaLeu 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pLeuGlnGlu...AsnTyrAspAsnCysGluIleValAlaPheValAlaA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTAC...TCAC 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValGluIleAlaArgLysValGlyAlaAspAlaLeuCysHisGlyCysTh 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euAlaProGluLeuThrValIleAlaProTrpArgIleTrpAsp..... 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTAC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rGlyLysGlyAsnAspGlnIleArgPheGlu...SerCysPheAlaAlaL 141
                                                                                                                                                        GCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAA 653
nGluProGluPheLeuThrileSerValValLysGly...GluIleThrA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    818.00
2.801
72.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1 to: 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 44.638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401
                                                                                                                                                                                                                          203
```

```
seq_name: sp_plant:Q9SZX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1054 TCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTC 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1004 GCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAGGTG 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1154 CAACTGATGCCACCGGGTTCATCAACATCAATTCCCTC.....AGGCTG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1104 TCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGC 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      854 CAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACC 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        804 CGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCC 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             754 ATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACAT 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 laValAsnGlyGluAlaMetSerProTyrAsnThr.....Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               704 TGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTC 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1198 AAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 rHisLeuValTyrAspGlyArgTrpPheThrProLeuCysAlaSerLeuL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              954 TGAGCTGGTGTATACCGGTTTTACGGCCTAGCCCTGAGTGTGAATTTGTCC 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 LeuAspLysThrThrArgLysTrpLysGlnThrValAlaAlaGluPheSe 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 rLeuTyrSerGluGluPheAlaThrPheGlyAspAspAsnValTyrAspG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 LysMetTyrLysGlySerValGlnAlaIleGlnLysLysSerProAsnSe 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 euAlaAlaGlyThrLeuAlaGluGluMetAsnGlyGluValIleVal 348
                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TremBLrel. 13, Created)
01-MAY-2000 (TremBLrel. 13, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE-LIKE PROTEIN (EC 6.3.4.5).
F617.40 OR AT4G24830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 lnSerHisAlaGluGlyPheIleArgLeuTyrSerLeuSerSerArgIle
                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399 Lys 399
                                                                                                                      Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R., Gielen J., Van Montagu M., Bancroft I., Hoheisel J., Mewes H.W., Mayer K.F.X., Schueller C.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9SZX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9SZX3
                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
                                        EU Arabidopsis sequencing project; submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGC 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           roGlyGlyThrValMetValGluAlaLeuArgGlyIleGluGluLeuVal 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              498 AA.
                                                                                                                                                                                                                                                                                                                                 core eudicots; Rosidae;
```

• ,

```
SO SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 815.00
Ratio: 2.890
Percent Similarity: 71.212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: Q9SZX3 from: 1 to: 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-775-693-1 x Q9SZX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL049657; CAB41123.1; -
EMBL; AL161562; CAB79393.1; -
InterPro; IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pfam; pf00764; Arginosuc_synth; 2.
proDom; pD003544; Arginosuc_synth; 1.
prOSITE; pS00564; ARGININOSUCCIN_SYN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 498 AA; 54880 MW; BCD9A856E5F50D5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 ValValLeuAlaTyrSerGlyGlyLeuAspThrSerVallleValProTr 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 pPheIlePheProCysLeuArgAlaGlyAlaIleTyrGluArgLysTyrL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 lyGlnGlyIleLysGluLeuGluGlyLeuGluGlnLysAlaLysAlaSer 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 GCCAGAAG...GAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 pLeuLysGluAsnTyrGlyCysGluValValCysPheThrAlaAspValG 161
                                                                                                                                                                                                                                                                                                                                          249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCAT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyAlaSerGlnLeuValValLysAspLeuThrGluGluPheValLysAs 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euLeuGlyThrSerMetAlaArgProValIleAlaLys..... 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCGCCCAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
AspMetTyrMetMetSerValAspProGluAspAlaProAspGlnProGl 315
                                                         GGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCCTGA 662
                                                                                                         euSerHisGluGlyAspLeuLeuGluAspProAlaAsnGluProLysLys 298
                                                                                                                                                                  TCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                           lProValThrLysLysSerIleTyrSerArgAspArgAsnLeuTrpHisL
                                                                                                                                                                                                                                                                                    CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                                                             GlnGlyArgGluAspAlaIleGluTyrAlaLysLysHisAsnValProVa 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                         luLeuLysValValAlaProTrpArgGluTrpGlu......Ile 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ......valArgPheGluLeuThrPhePheSerLeuAsnProG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 42.172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ........
                                                                                                                                                                                                                                          282
```

seq_name: sp_bacteria:Q9K4Y8 seq_documentation_block: 1163 CCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200 1113 TGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATG 1162 1063 AAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAA 1112 663 CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712 344 AsnThrIleGlyGlyLysHisGlyIleGlyArgIleAspMetValGluAs 360 713 TCAAGGATGGCACCACCCAGCCAGCCTCCTTGGAGCTCTTCATGTACCTG 410 lTyrAlaGlyArgTrpPheAspProLeuArgGluSerMetAspAlaPheM 427 394 GluSerIleGlnValLysAspThrLeuAlaLeuLysTyrAlaGluMetVa 410 863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG 912 813 CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAGCAGGCA 862 763 AACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAA 812 444 LysGlySerValSerValThrGlyArgGlnSerProAsnSerLeuTyrAr 460 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE 477 laAlaGlyPheIleArgLeuTyrGlyLeuProMetLys 489 460 gGlnAspIleSerSerPheGluGlySerGluIleTyrAsnGlnAlaAspA 477 MEDLINE-20158877; PubMed=10692366; Xu Y., Liang Z., Legrain C., Ruger H.J., Glansdorff N.; Xu Y., Liang Z., Legrain C., Ruger in the bacterial domain: Novel "Evolution of Arginine blosynthesis in the bacterial domain: Novel gene-enzyme relationships from psychrophilic moritella strains (vibrionaceae) and evolutionary significance of n-alpha-acetyl ornithinase."; Q9K4Y8; Q9K4Y8 -!- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC J. Bacteriol. 182:1609-1615(2000).
-j- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP + PYROPHOSPHATE + L-ARGININOSUCCINATE. NCBI_TaxID=111292; Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae; Moritella sp. 2693 ARGG. LIGASE). SEQUENCE FROM N.A. Moritella. uTyrIleGluIleGlyIleGluSerGlyLeuProValAlaLeuAsnGly. 331 GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGT 962LysAlaLeuSerProAlaThrLeuLeuAlaGluLeu 343 GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012 $hr {\tt IleLeuPheAlaAlaValGlnGluLeuGluSerLeuThrLeuAspArg}$ PRELIMINARY; 404 AA

```
alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY.

-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

C -!- SIMILARITY: TO THE ARGININOSUCCINATE SYNTHASE FAMILY.

R EMBL; AJ252021; CAB95033.1; -.

R InterPro; IPR001518; Arginosuc_synth.

Pfam; pF00764; Arginosuc_synth; 1.

JR ProDom; PD003544; Arginosuc_synth; 1.

DR PROSTITE; PS00564; ARGININOSUCCIN_SYN_1; 1.

DR PROSTITE; PS00564; ARGININOSUCCIN_SYN_2; 1.

DR PROSTITE; PS00565; ARGININOSUCCIN_SYN_2; 1.

KW ATP-binding; Arginine biosynthesis; Ligase; Urea cycle.

SQ SEQUENCE 404 AA; 44432 MW; 9E1C4D037AF5923F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: Q9K4Y8 from: 1 to: 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-775-693-1 x Q9K4Y8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
          601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC 650
                                               155
                                                                                      551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC 600
                                                                                                                           168 gAspIleProThrAlaAlaSerGlyThrLysIleTyrSerArgAspAlaA 185
                                                                                                                                                                   501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                               451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                    139 laLeuAlaProGluLeuThrValIleAlaProTrpArgIleTrpAsp... 154
                                                                                                                                                                                                                                                                                                                          401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                         304 CAAGTGGAAATCGCCCAGCGGGAAGGGGGCCAAGTATGTGTCCCACGGCGC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 ACCGCTACCTCGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 TGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 CTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 CCAACATTGGCCAG...AAGGAAGACTTCGAGGAAGCCCAGGAAGAAGGCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 lyThrTyrLeuLeuGlyThrSerMetAlaArgGlnSerIleAlaLysAla 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 LeuAlaSerGlyAlaSerGluCysTyrValValAspLeuLysAspGluLe 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 laAspValGlyGinGlyAlaGluGluLeuGluGlyIleGluAlaLysAla 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 pLeuGlnGlu...AsnTyrAspAsnCysGluIleValAlaLeuPheValA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 GCTGAAGGAACAAGGCTATGAC.....GTCATTGCCTATCTGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....LeuThrSerArgGluSerLeuLeuGluTyrLeuAlaGluAr 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      776.00
2.713
70.968
Length: 403
Gaps: 10
Percent Identity: 43.672
```

RA RA RA RA RA RA	R O C C C	DT DT DE	seq.	seq													
	Staph Bacte Bacil NCBI_	01-JU 01-JU 01-JU ARGIN ARGG	_documen: 099VC7	397 A	92	1150 . 380 s	1101 G 363 n	1051 (347)	330	951 313	97	851 280	801 263	751 247	701 232	651 218	202
SEQUENCE FROM N.A. SEQUENCE FROM N.A. (Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian Matsumaru H., Maruyama A., Murakami H., Hosoy Takahashi N.K., Sawano T., Inoue R.I., Kaito Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Yamashita A., Oshima K., Furuya K., Yoshino C Ogasawara N., Hayashi H., Hiramatsu K.,	ylococci ria; Fii lus/Stap TaxID=1	01-JUN-2001 (Tremblrel. 1 01-JUN-2001 (Tremblrel. 1 01-JUN-2001 (Tremblrel. 1 01-JUN-2001 (Tremblrel. 1 ARGININOSUCCINATE SYNTHAS ARGG OR SA0822.	ntation	rgIleLys sp bacter	AGGCTGAAG	р. Р.	FICTCTCT 	GTGTCCGTCCTCAACGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCCACT :::::: :: ValLysMetTyrLysGlySerValGlnAlaValGlnLysGlnSerProAs	TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG :: ::::::: :: euLeuAlaAlaGlyThrLeuAlaGluGluMetAsnGlyGluValIle	TGCTGAGG ::::: eSerHis1	ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT ::::: ::: :: ::: :::! ValleuAspLysIleThrArgLysTrpLysHisThrValAlaAlaGluPh	CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC ::: ::::: hrProGlyGlyThrValMetValGluAlaLeuArgGlyIleGluGluLeu	CATEGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 	TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCGTATTGA:::	AGGTGACCA. ::::: lulleThrA	CAACACC	GlnPros
I N.A. Ita T., Ii A., P. Maruya (., Sawa Kuhara Kuhara Oshima	aureumicutes ohylococ 58879;	(Trembl.) (Trembl.) (Trembl.) (Trembl.) INATE S) 22.	_block: PRELIMI	399 ia:09	G 1200	ACTGATG::: 	ACAATGA ::: yrSerGl	CCTCAAC : etTyrLys	ETGCATCO :::: :AlaAlac	CTGGTGTA ceuValTy	ACCGGGA/ ::: spLysIle	AGGCACC; : yGlyThr'	GAGAACC GluAsnA	ACCTGAA yrLeuAs	CAACGTC	CCTGACA :::: ProGlup	erLysG1
Uchiyan Noki K.I Noki K.I Ima A., Ino T., S., Got K., Fu	ıs subsp 3; Bacillu Cus group	rel. 17, rel. 17, rel. 17, cel. 17,	NARY;	9VC7		CCACCGG	.GGAGCTG ::: uGluPhe	GGCCAGG ::: Glyserv	CCAAGTO :: : : LyThrLe	ATACCGGT	AGTGCGC/ ::: ThrArgI	ATCCTTT: :::::: ValMetV:	GCTTCAT ::::: rgLeuVa	CGAAGTC nGluLys	CAACGTCAAGGATGGCA ::: rAlaValAsnGlyGluc	TTCTCGA::	roSerLysGlnValTrpThrMetThrValAs
la I., B ., Naga Murakam Murakam Inoue R O S., Y ruya K. iramats	lus/Clos lus/ Stap	Cr	PRT;			AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTC :: ::::: spGlnSerHisAlaGluGlyPheIleArgLeuTyrSerLeu	TCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTAT ::: ::::::::::::::::	TGTACAT alGlnAl	CCAGGAG uAlaGlu	:CTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGT :::::	AAAATCAA ysTrpLy	ACCATGCI ::: alGluAla	TGGAATG: : GlyMeti	GCGGGCA ::: AlaAlaA	GCACCACCCAC ::: luGluMetTyr	ACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGT :::::: ::::: GluProGluPheLeuThrIleSerValValLysGly	ThrMetT
iaba T., i Y., L ii H., H ii H., Ka ii I., Ka abuzaki , Yoshi	ıs N315. ostridium ophylococ	eated) st sequence st annotati	401			AACATCA :::::: ArgLeuT	TGAACGT ::::: heGlyAs	CCTCGGC ::: aValGln	CGAGTGG ::::::: GluMetA	CTAGCCC::: 	ACAAGGO ::: sHisThr	rcatttac LeuArgo	AAGTCCC LysSerAı	AGCATGG	CCACCAGACC' ::: tTyr	TTCAAAA ValvalL	hrValAs
Yuzawa ian J., osoyama ito C., J., Ka	m group	ce update) Lion update	AA.			ATTCCCT	GCAGGGT :::::: pAspAsn	CGGGAGT ::::: LysGlnS	AAGGGAA :: :: snGlyGl	TGAGTGT	CTGGGCT::::::	ACATCGA 	SAGGTATO	CGTGGGCC ValGly/	AGACCTCCTTG	AAGGGGTC ysGly	pProlleAs
uzawa H., Kobayashi I. n J., Ito T., Kanamori soyama A., Mizutani-Ui so C., Sekimizu K., r., Kanehisa M., c., Shiba T., Hattori	ŭ.	ite)				Serser	GATTAT. ValTyrA	CCCCACT	AGTGCAG : uValIle	TGAATTTG sAlaSerL	TGAAATT::: -::: laGluPh	AGGCCTTC	TACGAGA TyrGlu1	CGTATTG/ ::: argvalas	GAG	CCTGTG	pAlaP
bayashi , Kanam zutani- zu K., zu K., M.,						1191 396	1149 380	1100 363	1050	1000	950	900	850 280	4 800 1 3 263	C 750	A 700 : G 232	r 218
I., nori M., Ui Y.,																	

```
SQ RT RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-775-693-1 x Q99VC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: Q99VC7 from: 1 to: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE 401 AA; 44455 MW; BAA35E9F6C6FD5A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lancet 357:1225-1240(2001).
EMBL; AP003132; BAB42061.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 ACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 CCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 aValGlnTrpLeuIleAspLysGlyTyrAspValValAlaCysCysLeuA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 GlulleAlaGluLysThrAsnSerValGlyIleAlaHisGlyCysThrGl 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 GAAATCGCCCAGCGGGAGGGGGCCAAGTATGTCTCCCACGGCGCCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 MetGlyAlaValGluCysHisIleIleAspAlaThrLysGluPheSerAs 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 spValGlyGluGlyLysAspLeuAspIleValTyrLysLysAlaLeuAsp 51
                                                                                                                                                                                                                                                                                                                                                                                                               410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 yrProLeuValSerAlaLeuSerArgProLeuIleAlaLysLysLeuVal 101
                                                                                                                                                                                                                                                               510 CATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGC 559
                                                                                                                                                                                                                                                                                                                                       460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                                                                                                                                                                                                                                                            135 roserLeuLysalaPheAlaProValArgGluTrpAlaTrp....... 148
                                                                                                                                                                                      560 ACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCT 609
                                                                                                                                                                                                                             163 oValSerIleAsnHisAspSerProTyrSerIleAspGlnAsnLeuTrpG 180
                                                                                                                                                   180 lyargalaasndluCysGlyIleLeuGluAspProTyralaalaProPro 196
660 TGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCCTGTGAAGGTGACCA 709
                                                                               197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pGluTyrValSerTyrAlaIleLysGlyAsnLeuMetTyrGluAsnAlaT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                      yLysGlyAsnAspGlnValArgPheGluValAlaIleLysAlaLeuAsnP 135
                                                                                                                                                                                                                                                                                                  .....SerArgGluGluGluIleAspTyrAlaIleLysHisAsnIlePr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                           GluAspAlaPheAspLeuThrAsnAlaLeuGluGluThrProAspThrAl 213
                                                                                                                CCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCC 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     761.00
2.689
71.827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 39.848
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: sp_bacteria:Q9KNT8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 ......AspGlyLysThrTyrGluLeuAsp...AspLeuIleLeuThr 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    710 ACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATGTAC 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  760 CTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 LeuAsnAlaLeuAlaGiyLysHisGlyIleGlyArgileAspHisValGl 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1010 GCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAGGTGTCCGTC 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 uAsnArgLeuValGlyIleLysSerArgGluIleTyrGluAlaProAlaA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    810 GAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAGCAG 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1110 CAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTG 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1060 CTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTA 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 laGluValIleLeuLysalaHisLysalaLeuGluThrIleThrLeuThr 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    860 GCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGAC 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308 nLeuTyrAsnGlyLeuTrpPheSerProLeuThrAspSerLeuLysLeuP 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      960 GGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACT 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 LysaspValalaHisPheLysProIleIleGluLysGlnPheAlaGluGl 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1160 ATGCCACCGGGTTCATCAACATCAATTCCCTC 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 helleAspSerThrGlnGlnTyrValSerGlyAspValArgIleLysLeu 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 PheLysGlyAsnAlaIleValAsnGlyArgLysSerProTyrThrLeuTy 358
                                                                                                                                 STRAIN=EL TOR N16961 / SEROTYPE 01;
STRAIN=EL TOR N16961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Sellers P., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Frase C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 raspGluLysLeuAlaThrTyrThrLysGluAspAlaPheAsnGlnAspA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||::::|||||||:::||| :::|||
375 laAlaValGlyPheIleAspIleTyrGlyLeu 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9KNT8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9KNT8;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGASE).
                                        Nature 406:477-483(2000).

Nature 406:477-483(2000).

- i- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP + -i- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = TOSYNT PYROPHOSPHATE + L-ARGININOSUCCINATE.
                    -i- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                 cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCT 959
                                                                                                                   DNA sequence of both chromosomes of the cholera pathogen Vibrio
  PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 AA.
                                                                                                                                                                                                                                     Sellers P.,
```

```
alignment_block:
US-09-775-693-1 x Q9KNT8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Q9KNT8 from: 1 to: 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio: 2.674 Percent Similarity: 71.320
610 CCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCC 659
                                         187 isValserThrGluGlyCalLeuGluSerThrTrpAsnAlaProAsn 203
                                                                                560 ACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCT 609
                                                                                                                        170 oCysalaAlaSerLeuThrLysIleTyrSerArgAspAlaAsnAlaTrpH 187
                                                                                                                                                             510 CATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGC 559
                                                                                                                                                                                                      154 LeuArgSerArgGluAlaCysLeuAspTyrLeuAlaGluArgAsnIlePr 170
                                                                                                                                                                                                                                           460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                                                                                                                                                                   141 roAspLeuHisValileAlaProTrpArgGluTrpAsp...... 153
                                                                                                                                                                                                                                                                                                           410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                                                                                      124 yLysGlyAsnAspGlnValArgPheGluGlyAlaPheAlaAlaLeuAlaP 141
                                                                                                                                                                                                                                                                                                                                                                                                           360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 GiuileAlaArgLysValGlyAlaAspAlaLeuAlaHisGlyCysThrGl 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 GAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 ACCTCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 yrreuLeuGlyThrSerMetAlaArgProvalTleAlaLysAlaGlnVal 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 TTGGCCAG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 sGlutyrileTyrProThrLeuLysThrGlyAlaTyrTyrGluGlyLysT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 SerGlyAlaSerGluCysTyrIleValAspLeuLysGluGluPheValLy 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 alGlyGlnGlyAspGluGluLeuLysGlyValGluAlaLysAlaLeuSer 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 GCTGAAGGAACAAGGCTATGAC.....GTCATTGCCTATCTGGCCAACA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 pLeuLysGlu...AsnTyrAspCysGluValValAlaPheValAlaAspV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF0074; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
ATP-binding; Arginine biosynthesis; Complete proteome; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 GTGGTTCTGGCCTACAGTCGCGGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 ValvalValAlaTyrSerGlyGlyLeuAspThrSerValIleIleProTr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: TO THE ARGININOSUCCINATE SYNTHASE FAMILY. EMBL: AE004330; AAF95783.1; TIGR: VC2642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: HOMOTETRAMER (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 AA; 44465 MW; A65C73B442B5AF82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               751.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 41.878
```

```
OS
OC
OC
OX
RP
RP
RA
RA
RA
RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID Q9CC10 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: sp_bacteria:Q9CC10
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                          MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                STRAIN-TN;
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         Mycobacterium leprae
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1160 ATGCCACCGGGTTCATCAACATCAATTCCCTC 1191
                                                                                                                                                                                                                                                                              Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1110 CAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTG 1159
                                                                                                                                                                                                                                                                                                                                                                           ARGG OR ML1412
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9CC10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 isAlaGlyGlyPheIleArgLeuTyrSerLeu 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1060 CTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTA 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1010 GCATCGCCAAGTCCCAGGAGCGAAGTGGAAGGGAAAGTGCAGGTGTCCGTC 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 rSerGluAspPheAlaThrPheGlyAlaAspGluValTyrAspHisSerH 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 TyrLysGlyGinalaValAlaThrGlnLysArgSerAlaAsnSerLeuTy 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 laAlaAspGluLeuAlaLysAspValAsnGlyGluValValIleLysLeu 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 uValTyrAspGlyArgTrpPheThrProLeuArgGlnAlaValPheAlaA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           960 GGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACT 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 LysThrSerPheGluPheArgGluGluLeuGlyIleLysAlaSerHisLe 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             910 CGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCT 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 lyThrileIleMetGluAlaLeuArgAlaValGluGlnLeuValLeuAsp 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               860 GCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGAC 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 uAsnArgLeuValGlyMetLlysSerArgGlyCysTyrGluThrProGlyG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            810 GAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAG 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 LeuAsnGlnLysGlyAlaLysHisGlyValGlyArgIleAspIleValGl 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             760 CTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 ......AspGlyGluAla...MetThrProTyrAsnAlaLeuLeuTyr 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               710 ACGTCAAGGATGGCACCCACCCACCAGCCTCCTTGGAGCTCTTCATGTAC 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 aGluTyrvalThrLeuGlnValAlaHiSGlyGluValValAlaVal.... 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               660 TGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGAAGGTGACCA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 GluAspCysTrpValTrpThrValAspProGluGlnAiaProAsnGluAl 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 AA.
```

```
RA
RT
RT
DR
DR
DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-775-693-1 x Q9CC10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio: 2.422
Percent Similarity: 68.357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: Q9CC10 from: 1 to: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; AL583922; CAC30363.1; -.
Interpro; IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pfam; PF00764; Arginosuc_synth; 1.
probom; PD003544; Arginosuc_synth; 1.
pROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 GCCAG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 GCTG...AAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 pIleGlyLysGluThrSerHisGluValValAlaValValIleAspLeuG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 TCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 GlyAlaValGluAlaIleValValAspAlaArgAspGluPheAlaGluGl 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 AlaalaArgalaHisGlyGlySerIleValalaHisGlyCysThrGlyLy 122
                                                                                                                                                                                                                                                                                                                                                                                            313 ATCGCCCAGGGGGAGGGGGCCAAGTATGTGTCCCCACGGCGCCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 yTyrCysLeuProThrValLeuAsnAsnAlaLeuTyrMetAspArgTyrP 89
                                                                                                                                                                                                                                                                                                      363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                            139 spLeuGluIleLeuAlaProvalArgAspTyrAlaTrpThr....... 152
                                                                                                                                                                                                                                                                      413 AGATAAAGGTCATTGCTCCC......TGGAGGATGCCTGAA 447
                                                                                                                                                                                                                                                                                                                                                                                                                           89 roLeuValSerAlaIleSerArgProLeuIleValLysHisLeuValAla 105
                                                                                                                                                                                                             448 TTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCA 497
                                                                                                                                                                              153 .....ArgGluLysAlaIleAlaPheAlaGluGl 162
                                                                                                                   498 ACACGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATG 547
                                                                                       548 AGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAG 597
                            598 AACCAAGCGCCTCCAAGGTCTCTACACGAAGACCCAAGGACCCAAGCCAAAGC 647
                                                          179 lnasnvalTrpGlyArgalavalGluThrGlyPheLeuGluHisLeuTrp 195
196 HisalaProThrLysGluValTyrSerTyrThrAspAspProThrIleAs 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399 AA; 43915 MW; 3AD2BlD33EE50E7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           685.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               percent Identity: 37.440
```

```
seq_name: sp_archea:Q9UX31
    seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         698 TGAAGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAG 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 nTrpAsnThrProAspGluValIleValGlyPheGluHisGlyValProV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 648 CCCCAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTG 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 alserIle.....AspGlySer..ProValSerMetLeuGlyA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       798 TGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACG 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 lalleGluala LeunsnargargalaGlyalaGlnGlyvalGlyargLe 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 748 CTCTTCATGIACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTAT 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 uAspValValGluAspArgLeuvalGlyIleLysSerArgGluIleTyrG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274 lualaproGlyAlaMetValLeuIleThrAlaHisAlaGluLeuGluHis 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                848 AGACCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1048 CAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCC 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        898 TTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAA 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                948 ATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAAT 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 ValThrLeuGluArgGluLeuGlyArgPheLysArgGlnThrAspArgAr 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 gTrpAlaGluLeuValTyrAspGlyLeuTrpTyrSerProLeuLysThrA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1098 ACTGTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATT 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      998 TIGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTG 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1148 ATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :::::: |||||:::::: ::: |||||::::||| 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1198 AAGGAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357 aGluSerLeuTyrAspPheAsnLeuAlaThrTyrAspGluGlyAspThrP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 heAspGlnSerAlaAlaArgGlyPheValTyrVal.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386 .....TyrGlyLeuProSerLysLeuAlaAlaArg 395
                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5).
                                                                                                                                                                                                                                                                                                                                                                              Q9UX3:
STRAIN-DSM 1617 / P2; STRAIN-DSM 1617 / Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C., Confalonieri F., Curtis B., Duguet M., Erauso G., Faguy D., Gansterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C., Gushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q., Kushwaha N., Van Der Oost J., Young F., Zivanovic Y., Doollittle W.F., St Jean A., Yan Der Oost J., Young F., Zivanovic Y., Doollittle W.F., Ragan M.A., Sensen C.W.; "Gene content and organization of a 281-kbp contig from the genome of the extremely thermophilic archaeon, Sulfolobus solfataricus P2.";
                                                                                                                                                                                                                                             Sulfolobus solfataricus.
                                                                                                                                                                                                        NCBI_TaxID=2287;
                                                                                                                                                                                                                               Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                   406 AA.
```

Quality: 656.50

Percent Similarity: 68.274

Percent Similarity: 68.274

Percent Identity: 39.594

US-09-775-693-1 x Q9UX31

Align For Identity: Align For Identity: 39.594

Align seg 1/1 to: Q9UX31 from: 1 to: 406

Quality: 604.50

Length:

185

us-09-775-693-1.rspt

alignment_scores: GN OS OC OC OX RN RP RA RL RD RD seq_documentation_block:
ID 043348 PRELIMINARY; seq_name: sp_human:043348 Stoneking T., Langston Y., Ahrens C.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC003999; AAB96328.1;
InterPro; IPR001518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; 2.
ProDom; PD003544; Arginosuc_synth; 1. SEQUENCE SEQUENCE FROM N.A. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 043348;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL PROTEIN RG007J15.1 IN CHROMOSOME 7031 (FRAGMENT). Homo sapiens (Human). 1157 CTGAT......GCCACCGGGTTCATCAACATC 1182 1107 CTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAA 1156 382 eraspGluMetalaArgGlyPherleGluile 392 1057 GTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCT 1106 367 oTyrSerGluLys11eAlaSerTyrAsn...LysGlyTrpTyr...ProS 382 351 ValSerAsnGlySerPheArgIleValGlyArgGluSerGluTyrSerPr 367 1007 ACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGGAAAGTGCAGGTGTCC 1056 334 ysvalAlaAspGluMetAsnLysTrpIleSerGlyGluAlaLysValGlu 350 317 pLeuValTyrGlnGlyLeuTrpPheGluProLeuArgGluThrLeuHisL 334 957 GCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCC 1006 301 ThrProMetGluLeuArgPheLysArgHisIleAspGlnLeuTrpSerAs 317 907 GACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGA 956 284 laAlaLeuClyLeuIleTyrAlaHisIleAspLeuGluLysThrIleTyr 300 857 CAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATG 906 267 eGluAsnArgValValGlyPheLysSerArgGluValTyrGluValProA 284 807 GGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAG 856 251 PheLeuAsnLeuLysPheGlySerHisGlyPheGlyArgValGluHisI1 267 757 TACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGT 806 239 snGlyGluLys.....MetGluLeuAsnLysLeuValAsp 250 657 CCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCCTGTGAAGGTGA 706 707 CCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTCATG 756 222 sLysGluIleValSerIleGluPheSerAsnGlyValProThrAlaValA 239 166 AA; 18967 MW; 26B6A3ADCFEBFFAD CRC64;

`

```
RR RR OCC OCC PR
                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                          seq_name: sp_archea:Q9HMQ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: 043348 from: 1 to: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-775-693-1 x O43348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                           1182 CAATTCCCTCAGGCTGAAGGAATATCATCGTCTCCAGAGCAAGGTCACTG 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1082 TCGGCCGGGAGTCCCCACTGTCTCTACAATGAGGAGCTGGTGAGCATG 1131
                                                                                                                                                                                                                                                                                                                                                                1232 CCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1132 AACGTGCAGGGTGATTATGAGCCAACTGATGCCACCGGGTTCATCAACAT 1181
                                                                                                        ARGG OR VNG2437G.
Halobacterium sp. (strain NRC-1)
                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHETASE.
                                                                                                                                                                                                                                                                                                                                                                                         148 eAsnTyrLeuArgLeuLysGluTyrHisTyrPheGlnSerLysValThrV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1032 AGTGGAAGGGAAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCC 1081
MEDLINE=20504483; PubMed=11016950;
                 SEQUENCE FROM N.A.
                                                                                   Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 euSerGlnGluSerLeuLeuSerLeuTyrLysGluGluLeuValSerVal 131
                                                                           Halobacterium
                                                                                                                                                                                                                                                                                                                              165 alLys 166
                                                        NCBI_TaxID=64091;
                                                                                                                                                                                                                      29нмQ2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   982 AGCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCG 1031
                                                                                                                                                                                                                                          29HMQ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         932 AAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTACGGCCT 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               882 TTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAATCAAAC 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   832 TCCCGAGGTATCTACGAGACCCCCAGCAGCACCATCCTTTACCATGCTCA 88:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        782 ATGGCGTGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGAAG 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              732 CCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAGC 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       682 AAAAAAGGGTCCCTGTGAAGGTGACCAACGTCAAGGATGGCACCACCCA 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 AsnProGluCysLysSerValHisHisCysIleThrLysSerGlnGluG1 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 sGlnThrSerLeuGluLeuPheValTyrLeuAsnGluValThrGlyLysH 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LysLysGlyValProValLysValThr...IleLysMetAlaProProHi 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pLeuAspIleGluAspPheThrMetAspArgGluValHisLysIle.... 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.003
81.622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 67.568
                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                 396 AA.
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RA
RA
RA
RA
RA
RA
RA
RA
DR
DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: Q9HMQ2 from: 1 to: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-775-693-1 x Q9HMQ2
                                               481 .....ATGGAGTACGCAAAGCAACACGGGATTCCCA 511
146 yLeuThrArgGluTrpGluIleGluTyrAlaAlaGluArgAspLeuProV 163
                                                                                                 136 ......HisAspValCysAlaProValArgGluLeuGl 146
                                                                                                                                                                                                                                                404 TGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTAC 453
                                                                                                                                                                                                                                                                                               117 sThrGlyLysGlyAsnAspGlnLeuArgPheGlu....................... 128
                                                                                                                                                                                                                                                                                                                                                                                                    101 IleLeuSerValAlaGluAlaGluGlyCysAlaAlaLeuAlaHisGlyCy 117
                                                                                                                                                   454 AACCGGTTCAAGGGCCGCAATGACCTG......
                                                                                                                                                                                                                                                                                                                                    354 CACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCAC 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 CAAGTGGAAATCGCCCAGCGGGAAGGGGCCAAGTATGTGTCCCACGGCGC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 ACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 TGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 CTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 CCAACATTGGCCAGAAGGAA...GACTTCGAGGAAGCCCAGGAAGAAGGCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., "Genome sequence of Halobacterium species NRC-1."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 eAla...AlaLeuCysPheAspAlaValArgAlaAsnAlaThrTyrGlnG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPRO01518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; UNKNOWN_1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 ly...TyrProLeuGlyThrAlaLeuAlaArgProValIleAlaAspAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 AlaAlaLeuGlyValGluHis...HisValValAspAlaThrAlaGluPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 alAspValGlyGlnProAspAlaGluPheAlaAlaAlaArgGluThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 GGCTCCGTGGTTCTGGCCTACAGTGGCGGGCCTGGACACCTCG...TGCAT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
EMBL; AE005124; AAG20519.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 lProLeuLeuLysGluGluTyrGlyTyrAspAspValIleGlyValThrV 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GlyThrValAlaLeuAlaPheSerGlyGlyLeuAspThrThrValCysVa 20
                                                                                                                                                                                                .....AlaValTrpArgAlaSerAsp..... 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 AA; 41994 MW; 8DA8C2DCAD94D092 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      539.50
2.107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 424
Gaps: 14
Percent Identity: 33.255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
```

1156 ACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATA 1205 1112 ATGAGGAGCTGGTGAGCATGAACGTGCAG.....GGTGATTATGAGCCA 1155 1062 CAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACA 1111 196 aAspIleTyrAlaTrpThrAspAlaProSerGlyGluThrGlyThrValA 213 180 ArgSerValGluGlyGlyHisLeuGluGluProAspTyrGlnProProAl 196 562 ATCAGCTACGAGGCTGGAATCCTGGAGAACCCAAGAACCAAGCGCCTCC 611 662 ACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAAC 711 612 AGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCCAACACCCCCTG 661 322 LeuAspGluThrGlnSerAlaValSerGlyThrValThrIleAlaPheGl 338 812 ACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAGCAGGC 861 225AspGlyThrAlaMetGlu...ProValAlaLeuIleGluAlaLe 238 712 GTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTCATGTACCT 761 372 AlaAspAlaThrGly..... :: ::: :::|||::::|||:::::: ||||
355 eralaAspAlaAlaSerPheAsnThrGluThrValAlaGlyIleGluGln 371 338 uGlyGlyArgAlaArgProIleAlaArgGluSerGluHisAlaValTyrS 355 305 laTyrGluGlyValValGluHisProLeuMetAspAlaLeuAsnGlyTyr 321 962 TGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGC 1011 288 sAlaGluArgAspPheThrAlaAlaValSerGlnGlnTrpAlaGlnLysA 305 862 ACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCG 911 380 rHisGlyPheGlnSerArgLeu 387 912 GGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGG 961

.....valAlaLysTy 380

1206 TCATCGTCTCCAGAGCAAGGTC 1227

```
OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-775-693-1
1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             February 12, 2002, 12:44:27; Search time 1806.06 Seconds (without alignments) 11317.456 Million cell updates/sec
                                                  114:
115:
116:
117:
117:
119:
220:
221:
221:
23:
24:
25:
26:
27:
27:
28:
29:
30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1472140 seqs, 8248589755 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atgtccagcaaaggctccgt.....gcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                 gp_pr:*
                                                                                                                                                                                                                                                                                                                                                           gb_pat:*
gb_ph:*
                                                                                                                                                                                                                                                                                                                                                                                                                     gb_htg:*
                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_ba:*
                                                                                                                                                                                                                                    em_fun:*
em_hum:*
                                                                                                                                                                                                                                                                                                                                                                                                          p_in:*
                                                                                                                                                                       em_ov:*
em_pat:*
                                                                                                                                                                                               em_om:*
em_or:*
                                                                                                                                                                                                                                                                                                                                                                                  b_ov:*
                                                                                                                                                                                                                        em_in:*
                                                                                                                                                                                                                                                            em_ba:*
                                                                                                                                                                                                                                                                                               gb_sy:*
                                                                                                                                                                                                                                                                                                              gb_sts:*
                                                                                                                                                                                                                                                                                                                        gb_ro:*
                                                                                                                                                                                                                                                                                                                                                                                               b_om:*
           em_htg_rod:*
                                               em_htgo_rod: *
                                                                                                                                               em_p1:*
                                                                                                                                                            em_ph:*
em_htg_other:*
                        em_htg_inv:*
                                                              em_htgo_inv:*
                                                                         em_htgo_hum: *
                                                                                    em_vi:*
                                                                                                            em_sy:*
                                                                                                                        em_sts:*
                                                                                                                                    em_ro:*
                                     em_htg_hum:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2944280
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

a			C					C)	c	0 0)				C	C								O		c				a (o ()	C			C					- {	Result No.
45	44	43	42	41	40	ه م	υ υ •	ں د 7 د	א ני	η N	ں د) L	ა u ა ⊢	2 0	29	28	27	26	25	2 4	2 6	ა ⊦	7 5) L	ά (α	1 /	16	15	14	13	12	11	7 0	οα	> ~	10	· U	4.	٠ (۸ د	۱ د	- <u> </u>	ult No.
301.6	305.2	310.4	\vdash	32	325.6	5	19.	٦,	א מ	лο	5,00		лy	3.0	986.2	œ	988.2	1009.6	1011.2	1014	2 2	1016 6	2 6	. > -	1030	1030.4	31.	1032	1052.2	1052.8	1055.4	1055.4	1057 8	1058	1050	1067.8	۱.	F 0.5	1231	١,) F	1239	Score
24.3	24.6	25.1	25.4	5	26.3	ِ ٥	ا در ا ا	۷.	۱, د	44	ъ. т.	٠.	77 4	77.0	ع د	•	9.		1.6	۳ : 80		2.0	٠ د د	83. -		03.4	س د -	8 3 3 4	4.	5	5	5	J1 (0 0 7 0 4 4	η U	n 0) H	γ. α			٥ :	100.0	Query Match
41255	405	360	10138	336	10040	118103	81346	10007	179658	80	91346	とりつい	J 0) (106376	369	ω	160658	149752	1877	1645	1561	1/95	1495	200400	80108 67476T	96858	110716	1868	$\overline{}$	43	159687	5501	100	איכ	100356	9 0	1000) H	1505	07	25	
													٠,	۸ د														s N	9	9	N	9	N	. v	٥,	4 د	۱ -	JK	ى ر	0 (י ס	ِ و	DB
SPBC428	HUMDIA		AE00				AC021	AE00181	AC024		AC021		AC092	2001					⋗	HUMASA1F		MUSA				2 3	ζ,	AC008/1/	품		AC026357		AL353717	AC0731	AP00305	AC0095	DOMAGE TO SOLVE	AC027175	200715	BC00924	AK O.S	HSASD	ID
ALU34302 3. POlitice C	of the minimum meters	The occurr	_	duman argi	AE001924 Deinococc	•		Thermoto	25 Homo	ıman	Home	079046 Homo	3 Homo sap	8693 Homo sap	3705 Homo	O Homo	ACULZOUZ HOMO Sapi	3582 Homo	04616 Homo	5 Human a	2074 Mus	0 Mous		08 Nucl	Homo s	Human DN	666 Homo	ACOOO/1/ Homo sapi	Huillall a	OUU HOING	НОПО	311 Homo	Homo	Ното	7	50 Homo	8 Bovine	75 Homo	153 Homo	09243 Homo s	AK027126 Homo sapi	30 Human mF	Description

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1560) Bock,H.G., Su,T.S., O'Brien,W.E. and Beaudet,A.L. Sequence for human argininosuccinate synthetase cDNA Nucleic Acids Res. 11 (18), 6505-6512 (1983) Human mrna for argininosuccinate synthetase. $x_0.01630$ X01630.1 GI:28871

LOCUS DEFINITION

ACCESSION

RESULT

ALIGNMENTS

12-SEP-1993

HSASD

VERSION KEYWORDS

SOURCE

ORGANISM

Homo sapiens synthetase.

REFERENCE AUTHORS TITLE

FEATURES

MEDLINE JOURNAL

84015388

/organism="Homo sapiens" /db_xref="taxon:9606" Location/Qualifiers .1560

```
Вр
                                                                                                                                                                                                                                                                                                                                                                                                                          οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 1239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                               481
                                                                                     496
                                                                                                                         421
                                                                                                                                                              436
                                                                                                                                                                                                    361
                                                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                     241 gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     variation
                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                       gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                 atggagtacgcaaagcaacacgggattcccatcccggtcactccccaagaacccgtggagc 540
ATGGAGTACGCAAAGCAACACGGGATTCCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGC
                                                                                                                                                  AAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAG
                                                                                                                                                                        aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                          AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGA
                                                                                                                                                                                                                                                aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgcccacagga
                                                                                                                                                                                                                                                                                                   GCACTGTATGAGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                  AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGGGCCCAAAAAGGTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aaggaagacttcgaggaagccaggaaggacgctcgaagcttggggccaaaaagggtgttc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="G
1526. .15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="A is U in variant pAS2"
431 c 434 g 302 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /POOLEIL_id="CAA25771.1"
/POOLEIL_id="CAA25771.1"
/POOLEIL_id="CAA25771.1"
/POOLEIL_id="CAA25771.1"
/db_xref="GI:28872"
/db_xref="SIISS-PROT: P00966"
/translation="MSSKGSVVILAYSGGIDTSCILVWLKEQGYDVIAYLANIGQKEDFEBAKKALKLGAKKYFIEDVSREFVEEEISCYSLAPQIKVIAPREMPEFYNREFGRNDL
VEIAQREGAKYVSHGATGKGNDQYREELSCYSLAPQIKVIAPREMPEFYNREFGRNDL
VEIAQREGAKYVSHGATGKGNDQYREELSCYSLAPQIKVIAPREMPEFYNREFGRNDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="put. polyadenylation signal"
1537. .1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NINSLRLKEYHRLQSKYTAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHCIAKSQERVEGKVQVSVLKGQVYILGRESPLSLYNEELVSMNVQGDYEPTDATGFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPDILEIEFKKGVPVKVTNVKDGTTHQTSLELFMYLNEVAGKHGVGRIDIVENRFIGM
KSRGIVETPAGTILYHAHLDIEAFTMDREVRKIKQGLGLKFAELVYTGLRPSPECEFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEYAKQHGIPIPYTPKNPWSMDENLMHISYEAGILENPKNQAPPGLYTKTQDPAKAPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="polyadenylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="pot. polyadenylation signal"
1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="U is C in variant pAS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="argininosuccinate synthetase (aa 1-412)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="three tandem arginin codons"
76. .1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1239; DB 9; Length 1560; 100.0%; Pred. No. 4.1e-247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "pot. additional A in pAS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is A in variant pAS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                               480
                                                                                                                                                    495
                                                                                                                                                                                      420
                                                                                                                                                                                                                            435
                                                                                                                                                                                                                                                               360
                                                                                                                                                                                                                                                                                                                                                                               315
                                                                                                                                                                                                                                                                                                                                                                                                                                                        255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
```

Qy 밁 δÃ 밁 Ş B Š В ğ

```
REFERENCE
                                                                                                                                                                                                                                                                                                                                                 RESULT
AK027126
                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   γQ
                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ъ
                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                    VERSION
                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q_{Y}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΥ
                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
     TITLE
                                                                  JOURNAL
                                                                                     TITLE
                                                                                                                                                                                                  ORGANISM
                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                             1276 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAATAG 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1216 GGTGATTATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1081 ctcggccgggagtcccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1036 GTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901 accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           856 CATGGCGTGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          736
                                                                                                                                                                                                                                                                                                                                                                                                                                  99tgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCGGCCGGGAGTCCCCACTGTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTG 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCTACGAGACCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9tgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCACCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gacattetegagategagtteaaaaaaggggteeetgtgaaggtgaecaaegteaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCCAACACCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caagegeetecaggtetetacaegaagaeeeaggaeeeaggeeaaageeeeeaaeaeeeet 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGAT
            Unpublished (2000)

2 (bases 1 to 1975)

Sugano,S., Suzuki,Y., Ota,T., Obayashi,
Shibahara,T., Tanaka,T. and Nakamura,Y.
                                                                                   Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
Direct Submission
                                                                            NEDO human cDNA sequencing project
                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                       oligo capping; fis (full insert sequence). Homo sapiens human small intestine cDNA to mRNA, clone_lib:HSI \,
                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                      AK027126 1975 bp mRNA PRI 29-SEP-2000 Homo sapiens cDNA: FLJ23473 fis, clone HSI13532, highly similar to HSASD Human mRNA for argininosuccinate synthetase.
                                                                                                                                                                                                                clone:HSI13532.
                                                                                                                                                                                                                                                                 AK027126.1 GI:10440175
                                                                                                                                                  (sites)
                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                Primates;
                           Obayashi, M.,
                                                                                                                                                           Catarrhini; Hominidae;
                        Nishi, T., Isogai, T.,
                                                                                                                                                             ното
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            675
```

```
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Вp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                             Вþ
                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                               밁
                                                                                                                                                                                                                          Qy
                                                                                                                                                                   Š
                                                                                                                                          g
                                                                                   밁
                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                     Š
                            망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATC 541
                                                                                                                                                                                                                                                                                                                                                                                                                         602 AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGGGCCCAAAAAGGTGTTC 661
                                                                                                                                                                                                                                                                                                                                                                                                                                        121 aaggaagacttcgaggaagccaggaagaaggcactgaagcttgggggccaaaaaggtgttc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                           1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                                                                                                                                                                                                      301 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga 360
                            842 AAGGGGAACGATCAGGTCGGGTTTGAGCTCAGCTGCTCACTGGCCCCCCAGATAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (Br.mail:cdnaleims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                          902 GTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTG 961
                                                                                                                                                        421 gtcattgctccctggaggatgcctgaattctaccaccggttccaagggccgcaatgacctg 480
                                                                                 NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert International Trade and Industry of Biotechnology; cDNA library sequencing: Research Association for Biotechnology; cDNA library construction, 5 - 6 3'-end one pass sequencing: Departent of construction, 5 - 6 3'-end one pass sequencing: Departent of virology and Human Genome Center, Institute of Medical Science, virology and Human Genome Center institute.
601 caagegeetecaggtetetaeaegaagaeeeaggaeeeageeaaageeeeeaaeaeeeet 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agency).
                                                                                                                                                                                                                                                                                                                                                                                    aaggggaacgatcaggtccggtttgagctcagctgctactcactggcccccagataaag 420
                                                                                                                                                                                                                                                        AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGA 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   argininosuccinate synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="HSI13532"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="highly similar to HSASD Human mRNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="human small intestine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="HSI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.5%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "cloning vector pmE18SFL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         score 1232.6; DB 9
pred. No. 8.4e-246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9; Length 1975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
```

```
δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC009243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1142 GACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGAT 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       781 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 840
| 781 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 1321
| 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1202 GGCACCACCACCAGACCTCCTTGGAGCTCATGTAACCTGAACGAAGTCGCGGGCAAG 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661 gacattotogagatogagttoaaaaaaggggtocotgtgaaggtgaccaacgtoaaggat 720
                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1442 GTGTATACCGGTTTCTGGCACAGCCCTGAGTGTAATTTGTCCGCCACTGCATCGCCAAG 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1382 ACCATGGACCGGGAAGTGCGCAAAATCAAACGAGGCCTGGGCTTGAAATTTGCTGAGCTG 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  841 atctacqagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    901 accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1502 TCCCAGGAGCGAGTGGAAAGGGAAAGTGCAGGTGTCCTCCAAGGGCCCAGGTGTACATC 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1562 CTCGGCCGGGAGTCCCCACTGTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAG 1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1081 ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                961 gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1141 ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggcaccaccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens, argininosuccinate synthetase, clone MGC:3634
IMAGE:3010137, mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC009243.1 GI:14328058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (06-JUN-2001) National Institutes of Health, Mammalian Submitted (06-JUN-2001) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, Institute, Mammalian MD 20892-2590, Institute, MD 20892-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                            Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project_URL: http://mgc.nci.nih.gov
                                                                                                                   CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
DNA Sequencing by: Institute
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 1595)
                                                                                                                                                                                                                                                                                   cgapbs-remail.nih.gov
```

Greene, Mark Ketteman and Anuradha Madan

```
Дδ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
Best Local Similarity 99.6
Matches 1234; Conservative
                                                                501 GTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTG 560
                                                                                421 gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                              441 AÁGGGGAACGATCAGGTCCGGTTTGAGGTCAGGTGCTAGTCAGTGGCCCCCCAGATAAAG 500
                                                                                                                                              361 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                             381 AAACAAGTGGAAATCGCCCAGGGGGGGGGGGGGCGAAGTATGTGTCCCACGGCGCGCACAGGA 440
                                                                                                                                                                                                               301 aaacaagtggaaatcgcccagcgggggggggccaagtatgtgtcccacggcgccacagga 360
                                                                                                                                                                                                                                                          201 AAGGAÁGACTTCGAGGAAGCCAGGAAGAAGGCACTGAÁGCTTGGGGCCCAAAAAAGGTGTTC 260
                                                                                                                                                                                                                                                                                                                                                                                                           121 aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 CTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTGGCCAG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 10 Row: e Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Product "argininosuccinate synthetase"
/Protein_id="AAH09243.1"
/b_xref="GI:14328059"
/translation="MSSKGSVVLAVSGGLDTSCILVWLKEOGYDVIAYLANIGOKEDF
EEARKKALKKGAKKVFIEDVSREEVEEFIWPAIOSSALVEDRYLLGTSLARFCIARKO
PEEARCKYVSHGATGKONDOVRFELSCYSLAPOIKVIAPWRWPEFYNREKGRNDL
MEYAKGHGIPIPVFPKNPRSMDENHALSYEAGILENPKNOAPPGLYTKODDAKAPN
TPDILEIEFKGGVPVKVTNVKDGTTHGTSLEJEMVLNEVAKHGVGRIDIVENRFIGM
KSRGITETPAGTILYHAHDIEAFTMDREVRKIKGGLIGLKFAELVYTGTBHASPEGEFV
KSRGITETPAGTILYHAHDIEAFTMDREVRKIKGGLIGLKFAELVYTGFHISPEGEFV
NINSLRLEEVHRLOSKVTAK"

NINSLRLEEVHRLOSKVTAK"

440 g 312 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Muscle, rhabdomyosarcoma"
/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: porm7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="MGC:3634 IMAGE:3010137"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="LocusID:445"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.4%; Score 1231; DB 9; Length 1595; 99.6%; Pred. No. 1.9e-245; tive 0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
```

δ

δÃ В Ş Ъ δÃ В δõ Вb γ БР

REF A T T REF At	ACOL ACOL DEFT ACCH VERS KEYW SOUR	Db D	
ERE UTH OUR ERE THE			
33 4 E 23		y y y y y y y y y y y y y y y y y y y	Оу ДЬ ДУ
Mammalia: "McLazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 1 (bases I to 180838) 2 (bases I to 180838) 3 Birren, B., Linton, L., Nusbaum, C. and Lander, E. 4 (Unpublished Chromosome 17, Clone RP11-54103) 5 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,	ACC27153 180838 bp DNA N HOMO Sapiens chromosome 17 clone RP11-54103 map 17, WORKING DRAFT ACC27153 ACC27153 GI:7331447 HTG, HTGS_PHASE1; HTGS_DRAFT. HTMAN	661 gacattctcgagattcgagttcaaaaaaggggtcctAGGACCCAGG 741 GACATTCTCAGAATCGAGTTCAAAAAAGGGTCCAAGA 741 GACATTCTCAGAATCGAGTTCAAAAAAGGGTCCTTGAAAAAAGGGTCCCTTGAAAAAAGGGTCCCTTGAAAAAAGGGTCCCTTGAAAAAAGGGTCCCTTGAAAAAAGGGTCCCTTGAAAAAAGGGTCCCTTGAAAAAAGGGTCCCTTGAAACCTCCTTTGAACCTCTTTGAACCTCTTTGAACCTCTTTCATTAATAAAAAAGGGTCCTTTAATTAA	541 atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac 600

TITLE JOURNAL COMMENT

```
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Tliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Leboczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldirin, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Miranby, T., Marylo, T., Maryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA all repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Young, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960737 consensus quality: 158974 bases at least Q40 Consensus quality: 169058 bases at least Q30 consensus quality: 174233 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 179000; agarose-fp
Insert size: 178138; sum-of-contigs
Quality coverage: 3.6 in Q20 bases; agarose-fp
Quality coverage: 3.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: M13; M77815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L5602
Center clone name: 541_0_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                               7265 9123: contig of 1859 bp in length 9124 9223: gap of 100 bp 9224 10641: contig of 1418 bp in length 10642 10741: gap of 100 bp 110742 110442 - 100 bp
                11947 12046: gap of 100 bp 12047 1424: contig of 2378 bp in length 14425 14524: gap of 100 bp 14525 17721: contig of 3197 bp in length 17722 17821: gap of 100 bp 17822 20638: contig of 2817 bp in length 20639 20736: gap of 100 bp 20736: gap of 100 bp 20739 24557: contig of 3839 bp in length 2659 24557: config of 3839 bp in length
                                                                                                                                                                                                                                           10742 11946: contig of 1205
11947 12046: gap of 100 b
                                                                                                                                                                                                                                                                                                                                                                                                                       3416 3515; gap of 100 bp
3516 5368; contig of 1853 bp in length
5369 5468; gap of 100 bp
5469 7164; contig of 1696 bp in length
7165 7264; gap of 100 bp
   24568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 415: gap of 100 bp bp in length 1503: contig of 1088 bp in length 1504 1603: gap of 100 bp 100 bp in length 1604 3415: contig of 1812 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zainoun, J., Zimmer, A. and Zody, M.
24667: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of 315 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                              misc_feature
                                                                                                          misc_feature
                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92617 92716: gap of 100 bp
92717 101894: contig of 9178 bp in length
101895 101994: gap of 100 bp
101995 118357: contig of 16363 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118358 118457:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138889 138988: gap of 100 bp
138989 180838: contig of 41850 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85368 85467: gap of
85468 92616: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48557 48656:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43518 43617:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38146 38245:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33431 33530:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72674 72773:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment"
10742. ,11946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_end: T7
                                              /note="assembly_fragment"
33531. 38145
                                                                                                                                                                                                                              /note="assembly_fragment" 20739 .24567
                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment" 14525. .17721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
1604. .3415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP11-54103"
/clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29147: contig of 4480 bp in length 29247: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                          12047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment
                                                                                                                                 /note="assembly_fragment"
                                                                                                                                                                        24668
                                                                                                                                                                                                /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59933:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55204:
                   /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .180838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55104: contig of 6448 bp in length 204: gap of 100 bp 59833: contig of 4629 bp in length 33: gap of 100 bp 66011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330: gap of 100 bp
38145: contig of 4615 bp in length
45: gap of 100 bp
43517: contig of 5272 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             773: gap of 100 bp
79925: contig of 7152 bp in length
025: gap of 100 bp
85367: contig of 5342 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   933: gap of 100 bp
66011: contig of 6078 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33430: contig of 4183 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111: gap of 100 bp 72673: contig of 6562 k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138888:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92616: contig of 7149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17: gap of 100 bp
48556: contig of 4939 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .7164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5368
                                                                                                                .33430
                                                                                                                                                                               . 29147
                                                                                                                                                                                                                                                                                                                                                                                                                              .14424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ap of 100 bp
contig of 20431 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length
```

```
Вp
                                           Q
                                                                               B
                                                                                                                   Ş
                                                                                                                                                        B
                                                                                                                                                                                          õ
                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                            Вþ
                                                                                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                   망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 147253 AAGGAAGACTTCGAGGAAGCCAGGAAGAATGCACTGAAGTTTGGGGCTAAAAAAGGTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 147193 CTCCTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTACCTGGCCAACATTGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 147133 ATGTCCACCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCAGCCTGGACACCTCCTGCACC 147192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                              147551 GTCATTGCTCCCTGGAGGATGCCCAAATTCTACAACCAGCTCAAGGGCCTCAATGACCTG
                                                                        147611 ATGGAATATGCAAAGCAACACAGGATTCCCCATCCCGGTCACACCCAAGAACTCGTGGAGC
                                                                                                                                                                                                                  147491 AATGGGAACAATCAGGTCCGGTTTGAGCTCATTTGCTACTCACTAGCCCCCCAGATAAAG 147550
                                                                                                                                                                                                                                                                                         147431 AAACAAATGGAAATCACCCAGTGGAAGGGGGCCAAGTATATGTCCCACAGCACCACGGGA 147490
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 1161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                   541 atggatgagaacctcatgcacatcagctacgaggctggaatcctgggagaaccccaagaac 600
                                                                                         481 alggagtacgcaaagcaacacgggattcccatccccggtcactcccaagaacccgtggagc 540
                                                                                                                                                                                                                                                                                                                                                                                    241 gcactgtatgaggaccgctacctcctgggcacctctctttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 aaggaagacttcgaggaagccaggaaggaaggcactgaagcttgggggccaaaaagggtgttc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y Match 88.2%;
Local Similarity 93.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
ATGGACGAGAACCTCATGCATATCAGCTACGAGTCTGGAATCCTGGAGAACCCTAAGAAC
                                                                                                                                                                 9tcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                       aaggggaacgatcaggttcgggtttgagctcagctgctactcactggccccccagataaag 420
                                                                                                                                                                                                                                                                                                                aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga 360
                                                                                                                                                                                                                                                                                                                                                                 GCACTGTATGAGGACCGCTACCTTCTGGGCACCTCTC--GCCAGGCCCTGCATCGCCTGC 147430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctcgtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
118458. .13888
/note="assembly_fragment"
138989. .180838
/note="assembly_fragment"
a 35476 c 35898 g 54235 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
92717. .101894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
72774. .79925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment" 66112. .72673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment"
43618. .48556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
101995. .118357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
80026. .85367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment"
55205. .59833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :66011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .92616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .55104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .43517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1093; DB 2;
Pred. No. 3.4e-217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2701 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 180838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 w
~·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
   147730
                                                                                                                                                147610
```

```
REFERENCE
AUTHORS
                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 148270 GGTGATTATCAGCCAATTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qγ
                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC025175/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 148330 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAATAG 148368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 148210 CTTGGCCAGGAGTCCCCCACTGTCTCTACAAGGAGGAGCCGGTGAGCATGAACGTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 148150 TCCCAGGAGCAAGTGGAAAGGGAAAGTGCAGGTGTCCTCCGAGGGCCCAGGTGTACATC
                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 148090 GTGGATACCGGTTTCTGGTACAGCCCTGAGTGTGAATTTGTCTGCCACTGCATCGCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 147970 ATCTACCAGGCCCCAGCAAGCACCATCCTTTACCTCGCTCATTTAGACACCCAAGGCCTTC 148029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 147910 CAGGGTGTGGGCTGTATTGACATCATGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGG 147969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 147850 GGCACCACCACCAGACCTCATTGGAGCTCTTCATGTACCTGAACGAAGTCGTGGGCAAG 147909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΩV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 147790 GACATTCTCGAGATCGAGTTCAAAAAAGGAGTCCCTGTGAAGGTGACCAACGTCAAGGAT 147849
                                                                                                                                                                                                                                                           AUTHORS
TITLE
                                                                                                                                                                   TITLE
                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148030 ACCATGGGCCAGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGTTGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1201 gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1141 ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1081 ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            961 gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    901 accatggaccgggaagtgcgcaaaatcaaacgaggcctggggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         841 atctacgaggaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781 catggcgttgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         721 ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gacattctcgagattcgagttcaaaaaaggggttccctgtgaaggtgaccaacgtcaaggat
                          Center: Joint Genome Institute
Center Code: JGI
                                                                              Direct Submission
Submitted (07-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:7711790.
                                                                                                                                                                                  2 (bases 1 to 165439)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG HOMO Sapiens chromosome 5 clone CTD-2081C10, SEQUENCE, 20 ordered pieces.
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                    1 (bases 1 to 165439)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                         AC025175.3
                                                                         ·---Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                               HTGS_PHASE2; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:9256455
                                                                                                                                                                                                                                                                                                                    Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148149
```

```
BASE COUNT
                                                                                                                                                                                                                              FEATURES
                            Query Match
       Best Local Similarity
                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus quality: 151915 bases at least Q40
Consensus quality: 160797 bases at least Q30
Consensus quality: 160797 bases at least Q20
Estimated insert size: 164720; agarose-fp estimation
Estimated insert size: 164730; sum-of-contigs estimation
Quality coverage: 4.55 in Q20 bases; agarose-fp estimation
Quality coverage: 4.56 in Q20 bases; sum-of-contigs estimation
**NOTE: This is a 'working draft' sequence. It currently
**consists of 20 contigs. Gaps between the contigs
** are represented as runs of N. The order of the pieces
** is believed to be correct as given, however the sizes
** of the gaps between them are based on estimates that have
** This sequence will be replaced
** but has faithful and the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Summary Statistics
                                                                                                  45132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center clone name: CITB-H1_2081C10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center Project Name: 658711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by the finished sequence as soon as it is available and the accession number will be preserved.

1 774: contig of 774 bp in length
775 874: gap of unknown length
                                                                                                                                                                                                                                                                                                                                   154783
154883
156599
                                                                                                                                                                                                                                                                              161014
161114
                                                                                                                                                                                                                                                                                                                                                                                        140895
                                                                                                                                                                                                                                                                                                                                                                                                           140795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105679
105779
107018
                                                                                                                                                                                                                                                                                                                                                                                                                             136977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82352
99538
99638
                                                                                                                                                                                                                                                                                                                                                                                                                                              .36877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78033
78133
82252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       775
875
21898
21998
26273
26373
                                                                                         /clone="CTD-2081C10"
/clone_lib="CalTech human BAC library D"
32811 c 33426 g 52152 t 1918 other.
                                                                                                                                                  /chromosome="5"
                                                                                                                                                                 /db_xref="taxon:9606"
                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                         .165439
                                                                                                                                                                                                                                                                            154882: gap of unknown length
156598: contig of 1716 bp in length
156698: gap of unknown length
161013: contig of 4315 bp in length
161113: gap of unknown length
161113: gap of unknown length
       88.1%;
93.6%;
                                                                                                                                                                                                                                162823: contig of 1710 bp in length 162923: gap of unknown length 165439: contig of 2516 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10577
10701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21997: gap of unknown length 26272: contig of 4275 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  874: gap of unknown length 21897: contig of 21023 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig of 1239
gap of unknown
contig of 1538
Score 1091.4; DB 2; Length 165439; Pred. No. 7.3e-217;
                                                                                                                                                                                                                                                                                                                                                                             gap of unknown length contig of 13888 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                             gap of unknown length contig of 3818 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of unknown length
contig of 6041 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown length contig of 33824 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown contig of 6321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length of 2301 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
of 9870
                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 19299 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown length
of 17186 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 4119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown length of 7766 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                         1918 others
                                                                                                                                                                                                                                  in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                     in length
```

ORIGIN

```
멍
                                              QΥ
                                                                                  밁
                                                                                                                 QΥ
                                                                                                                                                       DЬ
                                                                                                                                                                                     QY
                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                          ρy
                                                                                                                                                                                                                                                                                             Вр
                                                                                                                                                                                                                                                                                                                                Ωy
                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 1160; Conservative
51654
                                                                                                                                                                                                               51774 ATCTACCAGGCCCAGCAAGCACCATCCTTTACCTCGCTCATTTAGACACCAAGGCCTTC
                                                                                                                                                                                                                                                                                  51834 CAGGGTGTGGGCTGTATTGACATCATGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGG
                                                                                                                                                                                                                                                                                                                                                     51894 GGCACCACCACCAGACCTCATTGGAGCTCTTCATGTACCTGAACGAAGTCGTGGGCAAG 51835
                                                                                                                                                                                                                                                                                                                                                                                                                      51954 GACATTCTCGAGATCGAGTTCAAAAAAGGAGTCCCCGTGAAGGTGACCAACGTCAAGGAT 51895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52013 CAAGCACCTCCAGGTCTCTACACGAAGA-CCAGGACCCGGCCAAAGCCCCCCAACACCCCT 51955
                  52073 ATGGACGAGAACCTCATGCATATCAGCTACGAGTCTGGAATCCTGGAGAACCCTAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52193 GTCATTGCTCCCTGGAGGATGCCCAAATTCTACAACCAGCTCAAGGGCCGCAATGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52313 AAACAAATGGAAATCACCCAGTGGAAGGGGGCCAAGTATATGTCCCACAGCACCACGGGA 5225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52371 GCACTGTATGAGGACCGCTACCTTCTGGGCACCTCTC--GCCAGGCCCTGCATCGCCTGC 52314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52491 AAGGAAGACTTCGAGGAAGCCAGGAAGAATGCACTGAAGTTTGGGGGCTAAAAAGGTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52551 CTCCTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTACCTGGCCAACATTGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52611 ATGTCCACCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCAGCCTGGACACCTCCTGCACC 52552
                                                                                                                                                                                                                                 841 atctacgaggacccaggaggcaccatcctttaccatgctcatttagacatcgaggccttc 900
                                                                                                                                                                                                                                                                                                    781 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 840
                                                                                                                                                                                                                                                                                                                                                                          721 ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601 caagegeetecaggtetetacaeggaagaeeeagggaeeeaggeeaaageeeeeaaeaeeeet 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541 atggatgagaacotcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacgggcgccacagga 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 gcactgtatgaggaccgctacctcctgggcacctctctttgccaggccctgcatcgcccgc 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 aaggaagacttcgaggaagocaggaagaaggcactgaagcttgggggccaaaaaggtgttc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                       gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag 1020
                                                                     GTGGATACCGGTTTCTGGTACAGCCCTGAGTGTGAATTTGTCTGCCACTGCATCGCCAAG 5159:
                                                                                                                                                                                                                                                                                                                                                                                                                                             gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9tcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGGGAACAATCAGGTCCGGTTTGAGCTCATTTGCTACTCACTAGCCCCCCAGATAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                               51715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52432
```

```
δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                       Q
                                                                                                                                                  Qy
                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
 δÃ
                                       Вþ
                                                                                                              망
                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                     Matches 1132;
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51414 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAATAG 51376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
130
                                                           121 aaggaagacttcgaggaagccaggaaggactgaagcttgaggctcgaaaaaggtgttc 180
                                                                                                                                                      61
                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGATTATCAGTCAATTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 51415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggtgattatgagccaactgatgccaccgggttcatcaactcaattccctcaggctgaag 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                  ctcgtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                        ATGTCCGGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGGGGCCTGGACACCTCCTGCATC 69
                                                                                                                                                                                                           atgtocagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                CTCGTGTGGCTGAAGGAGCAAGGCTATGACGTCATTGCCTACCTGGCCAACATCGGCCAG 129
                                       AAAGAAGACTTTGAGGAAGCCAGGAAGAAGGCGCTGAAGCTTGGGGGCCAAAAAGGTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine ASS mRNA encoding argininosuccinate synthetase, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 1398)
Dennis, J.A., Healy, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Draft entry and computer readable copy of sequence [1] kindly provided by W.E.O'Brien, 14-JUL-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dennis, J.A., Healy, \dot{P}, J., Beaudet, A.L. and O'Brien, W.E. Molecular definition of bovine argininosuccinate synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine liver, cDNA to mRNA, clone pASbl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            argininosuccinate synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M26198.1 GI:162696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOVASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90046714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              deficiency
                                                                                                                                                                                                                                                                                                                                                                                  329
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natl. Acad. Sci. U.S.A. 86, 7947-7951 (1989)
                                                                                                                                                                                                                                                                                                                                                                                  Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSGKGSVVLAYSGGLDTSCILVWLKEQGYDVIAYLANIGQKEDF
/translation="MSGKGSVVLAYSGGLDTSCILVWLKEQGYDVIAYLANIGQKEDF
EEARKKALKLGAKKVFIEDISKEFVEEFTWPAIQSSALYEDRYLLGTSLARPCIARKQ
VEIAQREGAKYVSHGATGKGNDQIRFELTCYSLAPQIKVIAPWRMPEEYNRFQGRNDL
MEYAKQHGIPVPVTPKNPWSNDENLMHISYEAGILENPKNQAPPGLYTKTQDPAKAPN
                                                                                                                                                                                                                                                                                                                                                                                                  NINSLRLKEYHRLQNKVTAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                     SPDMLĒIEFKKGVPVKVTNVGDGTTHSTALELFLYLNEVAĞKHGVGRIDIVENRFIGM
KSRGIYETPAGTILYHAHLDIEAFTMDREVRKIKQGLGLKFAELVYTGFWHSPECEFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAA30388.1"
/db_xref="GI:162697"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="argininosuccinate synthetase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     RHCIAKSQERVEGKVQVSVFKGQVYILGRESPLSLYNEELVSMNVQGDYEPVDATGFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1398 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1248
                                                                                                                                                                                                                                                                                                                                                                                405 c
                                                                                                                                                                                                                                                                                         86.2%;
91.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos.
                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                       Score 1067.8; DB 4; pred. No. 1.4e-211; 0; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                399 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                      265 t
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                            Length 1398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-1993
                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovoldea;
                                                                                                                                                                                                                                                                           Gaps
                                                   189
                                                                                                                                                                                                                                                                               0;
```

```
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                рь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΔÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Дb
                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Дb
                                                                                                                                                                      В
                                                                                                                                                                                                Qy
                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                     ρy
                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                             δõ
                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                     QY
                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                 QΥ
                                                                                                                                        δõ
망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190
                                                                                                                                                                         1030
                                                                                                                                                                                                   1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 gcactgtatgaggaccgctacctcctggggcacctctcttgccaggccctgcatcgcccgc 300
1210 GAATATCATCGCCTCCAGAACAAGGTCACCGCCAAATAG 1248
                                                                     1141 ggtgattatgagccaactgatgccaccgggttcatcaactcaattccctcaggctgaag 1200
                                                                                                                1090 CTTGGCCGGGAGTCCCCACTGTCCCTCTACAATGAGGAGCTCGTGAGCATGAACGTGCAG
                                                                                                                                1081 ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361
                                                                                                                                                                                                                                                                                                                                                                                                                                                            730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601
                                                                                                                                                                                                                                                                                      910
                                                                                                                                                                                                                                                                                                                                                                        841
                                                                                                                                                                                                                                                                                                                                                                                                                                781
                                                                                                                                                                                                                                970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgccacagga 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCACTGTACGAGGACCGATACCTCCTGGGCACCTCTCTCGCCAGGCCCTGCATCGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGCAGGTGGAGATCGCCCAGCGAGAAGGAGCCAAGTATGTGTCTCACGGCGCCACAGGA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       caagegeetecaggtetetacaegaagaeeeaggaeeeagceageeaaageeeeeeet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGACGAGAACCTGATGCATATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGAGTATGCGAAGCAACATGGAATCCCCGTCCCCAGTCACCCCCAAGAACCCCGTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCATCGCTCCCTGGAGGATGCCCGAGTTCTATAACCGCTTCCAGGGCCGCAACGATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                   catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gacattotogagatogagttoaaaaaaggggtocotgtgaaggtgaocaacgtoaaggat
                                                                                                                                                                                                                                                                                                    accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                           atotacyayaccccaycayycaccatcctttaccatyctcatttayacatcgayyccttc
                                                                                                                                                                                                                                                                                                                                                                                                    CACGGCGTGGGCCGCATCGACATCGTGGAAAACCGCTTCATCGGGATGAAGTCCCGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACATGCTCGAGATCGAGTTCAAGAAAGGGGTCCCCGTGAAGGTGACCAACGTCGGGGAT
                                                                                                                                                                     TCCCAGGAGCGCGTGGAAGGGAAAGTGCAGGTGTCCGTCTTCAAGGGCCAGGTGTACATC
                                                                                                                                                                                                                                            gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag 1020
                                                                                                                                                                                                                                                                                                                                            ATCTACGAGACCCCAGCGGGGACGATCCTTTACCACGCTCATTTAGACATCGAGGCCTTC
                        gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                           GTCTACACGGGTTTCTGGCACAGCCCCGAGTGTGAATTTGTCCGCCACTGCATTGCCAAG 1029
                                                                                                                                                                                                                                                                                     ACCATGGACCGGGAAGTGCGCAAAATCAAGCAAGGCCTCGGCTTGAAATTCGCCGAGCTG
                                                      GGAGACTACGAGCCGGTTGATGCCACTGGTTTCATCAACATCAATTCCCTCAGGCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    549
                                                                                                                                                                                                                                                                                                                         960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            609
                                                                                                                                                                                                                                                                                                                                                                                                              849
                                                                                                                                                                                                                                                                                                                                                                                                                                        840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             729
                                                                                                                                                                                                                                                                                                                                                      909
                                                                  1209
                                                                                                                                                                               1089
```

AC009550

```
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /ERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Karattas, A., Echoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J.J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassillev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                                                                              Quality coverage: 4.4 in Q20 bases; agarose-fp
Quality coverage: 4.6 in Q20 bases;
NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (27-AUG-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 20, 2000 this sequence version replaced gi:6006236. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 188356)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome, clone RP11-382M14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC009550.3 GI:7622313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; M7815; 100% of reads Sequencing vector: M13; M7815; 100% of reads Chemistry: Dye-primer-amersham; 4% of reads Chemistry: Dye-terminator Big Dye; 96% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 159465 bases at least Q40 Consensus quality: 175637 bases at least Q20 Consensus quality: 182085 bases at least Q20 Insert size: 194000; agarose-fp Insert size: 187356; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC009550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 188356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: L1662
Center clone name: 382_M_14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
                                               100 bp
4670: contig of 2872 bp
4671 4770: gap of 100 bp
4771 8967: contin ~ 6
                                                                                                                                  1 1698: contig of 1698 bp in length
1699 1798: gap of 100 bp
1799 4670: contig of 2872 bp in length
8 9067: gap
8 13012:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188356 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            op DNA HTG 20-APR-2
RP11-382M14, WORKING DRAFT SEQUENCE, 11
                                                             of 100 bp
contig of 4197 bp in length
      contig of 3945
                                         100
      ф
   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-2000
```

```
Db 121521 AAGGAAGACTTCCAGGAAGCCAGGAAGAAGGCACTGAAGCCTGGGGCCAAAAAGATGTTA 121580
                                                                                                                                                                                                            Db 121461 CTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTACCTGGCCAGCATTGGCCAG
                                                                                                                                                                                                                                                                                                                     QУ
                                                                                                                                                                                                                                                                              Db 121401 ATGTCCAGCAAAGGCTCTATAGTTCTGGCCTGCAGTGGCAGCCTGGACACCTTCTGCATC 121460
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                      Best Local Sir
Matches 1151;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
121641 ACACTGTATGAGGACCGCTACCTCCTGGGAACCTCTCTCGCCAGGCCCTGCATCACCCAC 121700
                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                        181
                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
              241 gcactgtatgaggaccgctacctcctgggcacctctctttgccaggccctgcatcgcccgc 300
                                                                                                                                                                                                                            61 ctcgtgtgggctgaaggaacaaggctatgacgtcattggcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                    1 atgtecageaaaggeteegtggttetggeetaeagtggeggeetggaeacetegtgeate 60
                                                                                      aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc 180
                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57641 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89198 117364: GOULTY - 100 bp
117365 117464: gap of 100 bp
117465 188356: contig of 70892 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48466 6700
67006 67105:
67106 8909
89098 89197:
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21257 29479: contig of 8223 bp in length 29480 29579: gap of 100 bp 29580 48365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48366 48465:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13013 13112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment"
117465. 188356
/note="assembly_fragment"
a 37359 c 35201 g 57123 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
89198. .117364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment"
29580. .48365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment"
4771 ...8967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment"
1799. .4670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-382M14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-ll Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .188356
                                                                                                                                                                                                                                                                                                                                                                     85.4%;
92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117364: contig of 28167 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 bp 100 bp 100 bp 21992 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65: gap of 100 bp 67005: contig of 18540 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48365: contig of 18786 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12: gap of 100 bp 21156: contig of 8044 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .13012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .89097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .67005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .29479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .21156
                                                                                                                                                                                                                                                                                                                                                                     Score 1058; DB 2;
Pred. No. 6.1e-210;
                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                        85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1032 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in length
                                                                                                                                                                                                                                                                                                                                                                                       Length 188356;
                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                            121520
```

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qγ
                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                рь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 121761 AAGGGGAATGATCAGGTCTGGTTTGAGCTCACCTGCTACTCGCTGGCCCCCACAGATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 121701 AAACAAGTGGAAGTCGCCCAGCGGGAGGGGGCCAAATATGTGTCCCCACGGCACCACGGGA 121760
                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                      DEFINITION
                                                                                     AP003057/c
VERSION
                 ACCESSION
                                                                          LOCUS
                                                                                                                                                                    122598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122001 CCAAGCGCCTCCAGCTCTCTACACGAAGACCCCAGGACCCCGGCCCAAAAACCCCCCAACACCCCC 122060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121941 CATGGACGAGAACCTCATGCACATCAGCTGCGAGGCTGGAATCCTGGAGAATCCCGAGAA 122000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121881 GACGGAATATGCAAAGCAACGCGGGATTCCCCACCCCGGTCACTCCCAAGAACCCGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121821
                                                                                                                                                                                                       1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggggccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacct 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccc-cagataaa 419
                                                                                                                                                              gtgtacatcctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatg 1131
                                                                                                                                                                                                                                                                                                                                                                                                                atcyccaaytcccaygaycyaytyyaagygaaaytyccayytytccytcctcaaygyccay 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACCATGTACCGGGAAGTGCACAAAATCAAACAATGCCGGGGCCTTGAAATTTGCTGAGCT 122360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCACAGCGTGGGCAATATTGCCATCGTGGAGAACCGTTTCATTGGAACGAAGTCCCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gcatggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgagg 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tgacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaagga 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccaagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccc 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gatggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggag
                                                                                                                                                                                                                                                                                                                  GTGTACATCCTTGGCTGGGAGTGCCC---CACTGTCTACAACGAGGAGCCGGTGAGCATG 122537
                                                                                                                                                                                                                                                                                                                                                                                              GGTGTATACTGGTTTCTGGCTTTCCGGCACAGCCCTGAGTGTGAATTTGTCCGCCACTGC 122420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggtgtataccggtttacggcct-----agccctgagtgtgaatttgtccgccactgc 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 caccatggaccgggaagtgcgcaaaatcaaacaaggcctggggttgaaatttgctgagct 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATCTACCGGGCCCCAGCAGCCATCCTTTGCTACGCTCATTTAGACATCGAGGCCTT 122300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tatctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggcctt 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGTGCCACCCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAA 122180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCCGTGAAGGTGACCAACGTCAAGGA
             HTG Homo sapiens chromosome 11 clone RP11-382M14 SEQUENCE, 20 unordered pieces.
AP003057.1
                                                    22-DEC-2000 map 11q, WORKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121940
                                                        DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preserved
```

```
Submitted (20-DEC-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Only in DataBase (2000) In press 2 (bases 1 to 190665) Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hor Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Direct Submission
                                  NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 190665)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Homo sapiens 190,665 genomic DNA of 11q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens DNA, clone:RP11-382M14.
as soon as it is available and the accession number
                                                                                                                                                                                                                                                                          Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 185978 bases at least 040
Consensus quality: 187598 bases at least 030
Consensus quality: 188368 bases at least Q30
Consensus quality: 188368 bases at least Q20
Insert size: 188765; sum-of-contigs
Quality coverage: 8.21x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: HumDraftll Center clone name: RP11-382M14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: PCR products; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://hgp.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: RIKEN Genomic Sciences Center(GSC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hong-Seog, P.,
and Sakaki, Y.
```

1 31506 contig of 31506 bp in length
31607 63890 contig of 27537 bp in length
63991 91527 contig of 27537 bp in length
10628 106175 contig of 14548 bp in length
115610 125111 contig of 9202 bp in length
115610 125112 contig of 9902 bp in length
1125212 133211 contig of 9902 bp in length
1149670 155266 contig of 9962 bp in length
1149670 155266 contig of 5290 bp in length
1153313 171081 contig of 5290 bp in length
165313 171081 contig of 5769 bp in length
165313 174820 contig of 3639 bp in length
174921 178093 contig of 3639 bp in length
178194 182424 contig of 3639 bp in length
188255 183733 contig of 3173 bp in length
189378 18909 contig of 4231 bp in length
189378 18909 189277 contig of 1209 bp in length
189378 is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 31506: contig of 31506 bp in length

```
FEATURES
                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                     misc_feature
                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142674 149569: contig or 100 bp
149570 149669: gap of 100 bp
149670 155266: contig of 5597 bp in le
155267 155366: gap of 100 bp
155367 160596: contig of 5230 bp in le
160597 160696: gap of 100 bp
160597 160696: gap of 4516 bp in le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106176 106275: gap of 100 bp 106276 115509: contig of 9234 bp in length 115510 115609: gap of 100 bp 115610 125111: contig of 9502 bp in length 125112 125211: gap of 100 bp 1052112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112 1252112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174821 174920: gap of 174921 178093: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125112 125211: gap of 100 bp
125212 133211: contig of 8000 bp
133212 133311: gap of 100 bp
133312 142573: contig of 9262 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178194 18242
182425 182524:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178094 178193: gap of
178194 182424: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171082 171181: gap of 171182 174820: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142574 142673: gap of 100 b
142674 149569: contig of 6896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189278 189377: gap of 100 1
189378 190665: contig of 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186909 187008: gap of 100 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183734 183833: gap of 183834 186908: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165213 165312: gap of
165313 171081: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91528 91627: gap of 100 bp
91628 106175: contig of 14548 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63891 63990:
63991 9152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31507 31606:
31607 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment" 63991. .91527
                             /note="assembly_fragment"
165313. .171081
                                                                                                                                       /note="assembly_fragment"
155367. .160596
                                                                                                                                                                                                                                                                                                              /note="assembly_fragment clone_end:SP6 vector_side:right"
133312. .142573
                                                                                                                                                                                                                                                                                                                                                                                                                              115610.
                                                                                                      /note="assembly_fragment"
                                                                                                                                                                                                    149670
                                                                                                                                                                                                                         /note="assembly_fragment"
                                                                                                                                                                                                                                                         142674.
                                                                                                                                                                                                                                                                           note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RP11-382M14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location,
'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .31506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .190665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32524: gap of 100 b
183733: contig of 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     990: gap of 100 bp
91527: contig of 27537 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06: gap of 100 bp
63890: contig of 32284 bp in
                                                                                                                                                                                                 .155266
                                                                                                                                                                                                                                                      .149569
                                                                                                                                                                                                                                                                                                                                                                      .133211
                                                                                                                                                                                                                                                                                                                                                                                                                           .125111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .106175
                                                                                                                                                                                                                                                                                                           .142573
                                                                                     .165212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of 100 bp i contig of 5769 bp i gap of 100 bp i contig of 3639 bp i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 bp
3173 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 bp
3075 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     đđ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
```

```
В
                         QΥ
                                                               DЪ
                                                                                             Qy
                                                                                                                               DЪ
                                                                                                                                                            Q
                                                                                                                                                                                               DЬ
                                                                                                                                                                                                                              δõ
                                                                                                                                                                                                                                                               Ъ
                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                              망
                                                                                                                                                                                                                                                                                                                                                            QY
                                                                                                                                                                                                                                                                                                                                                                                                망
                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ър
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ър
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 1151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51002 ACACTGTATGAGGACCGCTACCTCCTGGGAACCTCTCTCGCCAGGCCCTGCATCACCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51182 CTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTACCTGGCCAGCATTGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51242 ATGTCCAGCAAAGGCTCTATAGTTCTGGCCTGCAGTGGCAGCCTGGACACCTTCTGCATC 51183
                                                                                                                                                                                               50702
                                                                                                                                                                                                                                                               50762 GACGGAATATGCAAAGCAACGCGGGATTCCCACCCCGGTCACTCCCAAGAACCCCGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                50942 AAACAAGTGGAAGTCGCCCAGCGGGAGGGGGCCAAATATGTGTCCCACGGCACCACGGGA 50883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                               480
                                                                                                                                                                                                                                                                                                                                                               420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600 ccaagcgcctccaggtctctacacgaagacccaggacccaggccaaagcccccaacacccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                               720
                                                                                                                                                                                                                              540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 gcactgtatgaggaccgctacctcctgggcacctctctttgccaggccctgcatcgcccgc 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ctcgtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                               CATGGACGAGAACCTCATGCACATCAGCTGCGAGGCTGGAATCCTGGAGAATCCCGAGAA
                                                                                                                                                                                                                                                                                                                              GGTCATTGCTCCCTGAAGTATGCCCGAATTCTACAACCGGTTCAAGGGCCACAGTGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacgggcgccacagga 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaaggtgttc 180
                                                          tggcaccacccagccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaa
                                                                                                                                                                                                                catggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaa
                                                                                                                                                                                                                                                                                gatggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggag
                                                                                                                                                                                                                                                                                                                                            ggtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacct 479
                                                                                                                               CCAAGCGCCTCCAGCTCTACACGAAGACCCAGGACCCGGCCAAAAACCCCCCAACACCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGAAGACTTCCAGGAAGCCAGGAAGAAGGCACTGAAGCCTGGGGCCAAAAAGATGTTA 51063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
189378. .190665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment"
36353 c 36659 g 56251 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment"
187009. .189277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment clone_end:T7 vector_side:right"
183834. .186908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
178194. .182424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
182525. .183733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174921. .178093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.4%;
92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1058; DB 2;
Pred. No. 6.1e-210;
0; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1902 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 190665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                              599
                                                                                                                                                                                                                                                                                                                                                                                              50823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                             779
                                                               50523
                                                                                                                             50583
                                                                                                                                                                                                                                                                                                                              50763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
50463
                                                                                                                                                                                               50643
                                                                                                                                                                                                                                                               50703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω,
```

780 gcatggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgagg 839

```
οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              рь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC073169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /ERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Snoo
                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50402 TATCTACCGGGCCCCAGCAGCACCATCCTTTGCTACGCTCATTTAGACATCGAGGCCTT 50343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50462 GCACAGCGTGGGCAATATTGCCATCGTGGAGAACCGTTTCATTGGAACGAAGTCCCGAGG 50403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                840
                                                                                                                                             Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McBwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., Connor, T., O'Donnell, P., O'Nell, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Venna, G., Talamas, M., Vassiliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Venna, G., Talamas, M., Talamas, M., Talamas, M., Vassiliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Venna, G., Talamas, M., Talamas, M., Talamas, M., Talamas, M., Vassiliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Venna, G., Talamas, M., Talamas, M., Talamas, M., Talamas, M., Talamas, M., Vassiliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Venna, G., Talamas, M., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aggctgaaggaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aacgtgcagggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctc 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtgtacatcctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatg 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggtgtataccggtttacggcct-----agccctgagtgtgaatttgtccgccactgc 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caccatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagct 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGCTGAAGGAATATCATCGTCTCCAGAGCAAGGTCACTGCAAAATAG 49998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACGTGCAGGGTGATTATGAGCCAATTGATGCCACCGGGTTCATCAACATCAATTCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGTACATCCTTGGCTGGGAGTGCCC---CACTGTCTACAACGAGGAGCCGGTGAGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGTATACTGGTTTCTGGCTTTCCGGCACAGCCCTGAGTGTGAATTTGTCCGCCACTGC 50223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACCATGTACCGGGAAGTGCACAAAATCAAACAATGCCGGGGCTTGAAATTTGCTGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tatctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggcctt 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Submitted (09-JUN-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 201989)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, 19 unordered pieces. AC073169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 11 clone RP11-87E1 map 11, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens chromosome 11, clone RP11-87E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                             Young,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC073169.1 GI:8389521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 201989)
                                                                                                                Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201989 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-2001
                                         tor Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50283
                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 205000; agarose-fp Insert size: 200189; sum-of-contigs Quality coverage: 4.2 in Q20 bases; Quality coverage: 4.3 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 189508 bases at least Q30 Consensus quality: 195790 bases at least Q30 Consensus quality; 195790 bases at least Q30 Consensus quality; 198358 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                        164545 164644: gap of 164645 201989: contig of
                                                                                                                                                                                                                                                                                                                                                                          109756
                                                                                                                                                                                                                                                                                                                                                                                                           109656 109755:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66613
66713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16062 16161:
16162 2116
21162 21261:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: WIBR
                                                                                                                                                                                                                                                                                           135850
                                                                                                                                                                                                                                                                                                                            135750 135849: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92046 92145:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78574 78673:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46163 46262:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34819 34918:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26220 26319:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12380 12479:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7646 7745: gap of 100 bp

7746 12379: contig of 4634 bp in length

12380 12479: gap of 100 bp

12380 12479: gap of 3582 bp in length

16061: contig of 3582 bp in length

16062 16161: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 1275: contig of 1275 bp in length
1276 1375: gap of 100 bp
1376 2986: contig of 1611 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4669 4768: gap of
4769 7645: cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1376 2986: contig of 1611 bp in length
2987 3086: gap of 100 bp
3087 4668: contig of 1582 bp in length
                                                                               /organism="Homo sapiens"
                                             /db_xref="taxon:9606"
                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41047:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66712:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56687:
                                                                                                                                                                                                                                                                                                                                                                                                                                    7712: gap of 100 bp 78573: contig of 11881 bp in length 1673: gap of 100 bp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cont
(46162: 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34818: contig of 8499 bp in length 918: 9ap of 100 bp 40947: contia of 77 bp
                                                                                                                                                                                                                                                                                       164544: contig of 28695 bp in
                                                                                                                                                                                                                                                                                                                                                              9755: gap of 100 bp 135749: contig of 25994 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262: gap of 100 bp
55587: contig of 10325 bp in length
687: gap of 100 bp
66612: contig of 9925 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2116: contig of 5000 bp in length
261: gap of 100 bp
26219: contig of 4958 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p of 100 bp contig of 5115 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 2877 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87_E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L10271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100
                                                                                                                                                                                                            100 bp
                                                                                                                                                                                                                                                                                                                        100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bases; sum-of-contigs
```

agarose-fp

bp in length

. .

```
밁
                                                                                                                                         QΥ
                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
DЪ
                         QΥ
                                                      В
                                                                                 δÃ
                                                                                                                                                                                                  δõ
                                                                                                                                                                                                                                日
                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 1151; Conserv
                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                 196726
                                                                                                                                                                        196666
                                                                                                                                                                                                                                196606
196846
                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                            121
                                                                                                                                                                                   61 ctcgtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                             gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                      aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaaggtgttc
                                                                                                               AAGGAAGACTTCCAGGAAGCCAGGAAGAAGGCACTGAAGCCTGGGGCCCAAAAAGATGTTA 196785
                                                                                                                                                                       CTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTACCTGGCCAGCATTGGCCAG 196725
ACACTGTATGAGGACCGCTACCTCCTGGGAACCTCTCTCGCCAGGCCCTGCATCACCCAC
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment" 21262. .26219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment"
16162 ...21161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
4769. .7645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="11"
/clone="RP11-87E1"
/clone=_lib="RPCI-11 Human Male
                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment"
164645. .201989
/note="assembly_fragment"
.37765 c 36760 g 60255
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
135850. .164544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment"
109756. .135749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment"
78674. .92045
/note="assembly_fragment"
92146. .109655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
66713. .78573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment"
56688. .66612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment
clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vector_side:right"
41048. .46162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
26320. 34818
/note="assembly_fragment"
34919. 40947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
12480. .16061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
3087. .4668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment"
1376. .2986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                    85.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .12379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .56587
                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                       Score 1058; DB 2;
Pred. No. 6e-210;
0; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                             H
                                                                                                                                                                                                                                                                                                                                                                             1805 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAC"
                                                                                                                                                                                                                                                                                                                   Length 201989;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                    120
                                                                                                                                          180
                            300
                                                                                  240
196905
                                                       196845
```

RESULT 10 AL353717/c

AL353717

155019 bp

DNA 9 C

NA HTG clone RP11-562M8,

05-AUG-2001 SEQUENCING IN

VERSION KEYWORDS

ACCESSION DEFINITION LOCUS

Homo sapiens chromosome 9 clone F PROGRESS ***, 3 unordered pieces. AL353717 AL353717.9 GI:15131977 HTG; HTGS_PHASE1; HTGS_ACTIVEFIN;

HTGS_ACTIVEFIN; HTGS_DRAFT;

HTGS_FULLTOP

```
밁
                                                                                                                                                                  Qy
                                                                                                                                                                                                                 Ωy
                                                                                                                                                                                                                                         DЬ
                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                       Вр
                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                    Вb
                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                  Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                      δÃ
                                                                     Qγ
                                                                                                                    20
                                                                                                                                                                                           DЬ
                                                                                                                                                                                                                                                                                                                                     рЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197026
  197803
                                                                                                                                            197626
                                                                                                                                                                                            197566
                                                                                                                                                                                                                                            197506
                                                                                                                                                                                                                                                                                        197446
                                                                                                                                                                                                                                                                                                                                      197386
                                                                                                                                                                                                                                                                                                                                                                                     197326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197086
960
                                                                                                                                                                                                                                                                  900
                                                                                                                                                                                                                                                                                                               840
                                                                                                                                                                                                                                                                                                                                                             780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                               gtgtacatcctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatg
                                                                                                                                                          tgacattctcgagatcgagttcaaaaaaaggggtccctgtgaaggtgaccaacgtcaagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccaagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATGGACGAGAACCTCATGCACATCAGCTGCGAGGCTGGAATCCTGGAGAATCCCGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            catggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACGGAATATGCAAAGCAACGCGGGATTCCCACCCCGGTCACTCCCAAGAACCCCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTCATTGCTCCCTGAAGTATGCCCGAATTCTACAACCGGTTCAAGGGCCCACAGTGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGGGGAATGATCAGGTCTGGTTTGAGCTCACCTGCTACTCGCTGGCCCCCACAGATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccc-cagataaa
                                                                                              GTGTACATCCTTGGCTGGGAGTGCCC---CACTGTCTACAACGAGGAGCCGGTGAGCATG
                                                                                                                                             GGTGTATACTGGTTTCTGGCTTTCCGGCACAGCCCTGAGTGTGAATTTGTCCGCCACTGC
                                                                                                                                                                                                       ggtgtataccggtttaccggcct-----agccctgagtgtgaatttgtccgccactgc
                                                                                                                                                                                                                                         CACCATGTACCGGGAAGTGCACAAAATCAAACAATGCCGGGGCTTGAAATTTGCTGAGCT
                                                                                                                                                                                                                                                       caccatggaccgggaagtgcgccaaaatcaaaccaaggcctgggcttgaaatttgctgagct
                                                                                                                                                                                                                                                                                                                                                                                                                                  TGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCCGTGAAGGTGACCAACGTCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAAGCGCCTCCAGCTCTACACGAAGACCCAGGACCCGGCCAAAACCCCCAACACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gatggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggag
                                                                                                                      1131
                                                                                                                                                                                                                    1011
                                                                                                                                                                                                                                                                   959
                                                                                                                                                                                                                                                                                                                                                               839
                                                                                                                                                                      1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       539
                                                                                                                                              197685
                                                                                                                                                                                            197625
                                                                                                                                                                                                                                            197565
                                                                                                                                                                                                                                                                                           197505
                                                                                                                                                                                                                                                                                                                                       197445
                                                                                                                                                                                                                                                                                                                                                                                     197385
                                                                                                                                                                                                                                                                                                                                                                                                                                     197325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360
                                                                                               197742
                                                  197802
```

```
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                        Best Local Similarity Matches 1146; Conserv
                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemistry: Dye-terminator ET-amersham; 0% of reads Chemistry: Dye-terminator Big Dye; 99% of reads
Chemistry: Dye-primer-amersham; 0% of reads
Chemistry: Dye-primer-amersham; 0% of reads
Consensus quality: 154590 bases at least Q40
Consensus quality: 154545 bases at least Q30
Consensus quality: 154709 bases at least Q20
Insert size: 154819; sum-of-contigs
Insert size: 154819; sum-of-contigs
Insert size: 15528; 7.3% error; agarose-fp
Quality coverage: 8.29x in Q20 bases; sum-of-contigs Quality
coverage: 7.89x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 0% of reads
Sequencing vector: plasmid; L08752; 99% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced gi:15131481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: bA562M8
----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sehra, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                       42308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 155019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117004 117103: gap of 100 bp
117104 155019: contig of 37916 bp in length.
Location/Qualifiers
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97615 97615: contig of 97615 bp in length
97616 97715: gap of 100 bp
97716 117003: contig of 19288 bp in length
                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---- Genome Center
                                                                                                                                                                                                                                            /note="assembly_fragment:02543
fragment_chain:1"
a 31372 c 33444 g 47694 t
                                                                                                                                                                                                                                                                                                                           97716...117003
/note="assembly_fragment:01189
fragment_chain:1"
117104...155019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment:03117
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP11-562M8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .155019
                                                                                                                            85.4%;
                                                                                                        0;
                                                                                                Score 1057.8; DB 2;
Pred. No. 6.9e-210;
Pred. No. 6.9e-210;
                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                    201 others
                                                                                                     Indels
                                                                                                                                                   Length 155019;
                                                                                                     6; Gaps
                                                                                                     w
••
```

```
JOURNAL REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    γΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC087311/c
                                                                                                                                                                                                 AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                           TITLE
AUTHORS
                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64199 GAATGTCA---TCTCCAGAGCAAGGTCACTGCCAAACAG 64164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1201 gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen, 2., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Cayle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karisson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Karisson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Karisson, E., Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Loulsey, E., Lucier, R., Luna, R., Martindale, A., Martinez, E., Massey, E., Mawbiney, E., McLeod, M.P., Mardindale, A., Martinez, E., Massey, E., Mawbiney, E., McLeod, M.P., Mardindale, A., Martinez, E., Massey, E., Mawbiney, E., McLeod, M.P.,
                                                                                                                                                                                                                                                                                                                                                                           Meador, M., Mei, G., Merscher, S., Metzker, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shoshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stone, H., Stone, H., Sutton, A., Syatek, A., Tabor, P., Tamerisa, A., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Walliams, G., Williamson, A., Washington, C., Watlington, S., Williams, G., Williamson, A., Stone, R., Kucherlapati, R., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Allsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenher, Kr., BRomin,D., Bouck,J., Benton,B., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACO87311 159687 bp DNA
Homo sapiens 12 BAC RP11-267D19 (Rosw
Human BAC Library) complete sequence.
                                                                                                             Submitted (25-DEC-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                    of Molecular and Human Genetics, Baylor
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                      Worley, K.C
                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC087311.22 GI:14277201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 159687)
                                                                                                                                                                                                                                                                          (bases 1 to 159687)
                                        (bases 1 to 159687)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RP11-267D19 (Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barbaria, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
```

Worley,K.C. Direct Submission
Submitted (05-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 1, 2001 this sequence version replaced gi:14190590. Direct Submission
Submitted (01-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jun 1, 2001 this sequence version replaced gi:14190590. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu (bases 1 to 159687)

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are o sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing. are only

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-9 of a local database that includes entries from dbSTS, local mapping efforts. 7:541-550) searches GDB, and

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage. SEQUENCING READ COVERAGE: Sequencing is completed to a minimum

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation

QUALSTAT-REPORT---

2001 1801 1601 # 1401 bases 1201	Distribution of Quality < 40 Bases	Position Original+Context Edi	Contig length: Phrap values in estimate: Average error rate (BCM-Phrap estimate): Fraction of Phrap values less than 40: Number of consensus changing edits: Number of N's in consensus:
* *		Edited+Context	160224 159430 1.12363e-05 0.00137364

S

FEATURES

Version:

1.01 qxfo

source

repeat_region

```
complement(11501. .11569)
/rpt_family="MIR"
complement(11571. .12240)
                                                                                                                            complement(12242. .12407)
/rpt_family="MIR"
                                                                                                                complement(12510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="MLT1-INTERNAL" 2421. .2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="AluSx"
1056. .1403
                                                                                         /rpt_family="Alusx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="L1MEc"
34. .137
                                                                                                                                                  rpt_family="MER21B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /standard_name="139279"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP11-267D19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                    rpt_family="GA-rich"
                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'rpt_family="L1MEc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="L1MEc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   _family="AT_rich"
                                                                                                                                                                                                                           _family="L1PBa"
                                                                                                                                                                                                                                                                                                                                                    _family="L1PBa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _family="MLT1D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _family="L1ME1"
                                                                                                                                                                                                                                                                                                 _family="pTR5"
                                                                                                                                                                                                                                                                                                                                                                           _family="L1PBa"
                                                                                                                                                                                                                                                                                                                                                                                                   _family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _family="MLT1-INTERNAL"
                                                                                                                                                                                                                                                    .ly="AluSg"
                                                                                                                                                                                                                                                                             .y="L1PBa"
                                                                                                                                                                                                                                                                                                                            .y="L1PBa"
                                               Score 1055.4; DB 9;
Pred. No. 2.2e-209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phrap Value Range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                                                           DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30
                                                   Indels
                                                                        Length 159687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40
                                                  8; Gaps
                                                  ω
                                                                                  Qy
                                    δõ
                                                            Ъ
                                                                                                             Дb
                                                                                                                                   Qy
                                                                                                                                                               В
                                                                                                                                                                                     δÃ
                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                              р
                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              рь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ρy
                                                                                                                                                                                                              54778
                                                                                                                                                                                                                                                                                                                                                                                                               55011
              54538
                                                                                                               54658
                                                                                                                                                                54718
                                                                                                                                                                                                                                                                54838
                                                                                                                                                                                                                                                                                                               54898
                                                                                                                                                                                                                                                                                                                                                               54957
                                                                                                                                                                                                                                                                                                                                                                                                                                                               55071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55251 AAGGGGAGCGATCAGGTCCAGTTTGAGCTCAACTGCTACTCGCTGGCTCCCCAGATAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55490 AAGGAAGATTTCAAGGAAACCAGGAAGAA-GCATTGAAGCTTGGGGGCCAAAAAGGTGTTC
           55371
                                                                                                                                      961
                                                                                                                                                                                                                                                                                                                                                                                       661
                                                                                                                                                                                                                                                                                       781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtgtataccggtttacgyccctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                          accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                          atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                           atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACGGCGTGGGCCGTACTGACATCGTGGAGAACCGCTTTATTGGAATGAAGTCTCGAGGT
                                                                                                                                                                                                                                                                           catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 840
                                                                                                                                                                                                                                                                                                             GGCTCCACCTACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAA 54839
                                                                                                                                                                                                                                                                                                                        99caccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                        caagogoctocaggtototacaogaagacocaggacocaggocaaagcococaacacocot 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaggaagacttcgaggaagccaggaagaaggcactgaagcttgggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                             ACCATGGACTGGGAAGTGCACAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTG
                                                                                                                                                                                                              ATCTAGGAGGCCCCGGCAGGCACCATCCTTTACCACGCTCATTTAGACATCAAGGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                             CAAGCGCCTCCAGGTCTCTACGCGAAGACCCCAGGACCC-----GGCCCCCAACACCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAACAAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAATCCCAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGAATACGCAAAGCACCACGGGATTCCCATCCTGGTCACTCCCAAGAACCTGTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCCTGTAGCTGAAGGAACAAGGCTATGATGTCATTGCCTACCTGGCCAACATTAGCCAG
                                                            54539
                                                                                                             54599
                                                                                                                                                                                                                                                             54779
                                                                                                                                                                                                                                                                                                                                     780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480
                                                                                     1080
                                                                                                                                      1020
                                                                                                                                                             54659
                                                                                                                                                                                      960
                                                                                                                                                                                                             54719
                                                                                                                                                                                                                                      900
              54479
                                                                                                                                                                                                                                                                                                                                                                                                             54958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55312
```

55012 600 360

300 55372 180 55491 120

repeat_region repeat_region repeat_region repeat_region repeat_region

.3992

B Ş

55610

Query Match Best Local Similarity

85.2%; 92.4%;

repeat_region repeat_region

_famil

.6578

_fami

_famil

Matches

1145;

Conservative

0;

```
JOURNAL REFERENCE
                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC026357/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1201 gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dayy-Carroll, L. Dederich, D. A. Delaney, K. R. Delgado, O.,
Denn, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Draper, H.,
Dugan-Rocha, S., Durbin, K. J., Earnhart, C., Edgar, D., Edwards, C.C.,
Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, M., Ford, J.,
Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,
Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S.,
Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
Hernandez, J., Hernandez, O., Hodyson, A., Hogues, M., Holloway, C.,
Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Jaudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulseged, H., Lozado, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M.,
Merid, G., Metzker, M., Mner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N.,
Nguyen, A., Nguyen, N., Neal, D., Newtson, J., Newtson, N.,
Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
Peery, J., Peters, L., Peters, L., Pickens, R., Primus, E., Pu, L.,
Ouiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfs, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAATATCATCATCTCCAGAGCAAGGTCACTGCCAAATAG 54380
               Submitted (22-MAR 2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jan 8, 2001 this sequence version replaced gi:12043803.

Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R. Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Williams, G., Williamson, A., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Chen, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Chen, R., Davila, M.D., Davis, C., Chen, R., Davila, R., Davila, M.D., Davis, C., Chen, R., Davila, R., Davila, M.D., Davis, C., Chen, R., Davila, M.D., Davis, C., Chen, R., Davila, M.D., Davis, C., Chen, R., Davila, M.D., Davila, M.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratinge,H.C., Are,J.R., Banks,T., Barbaria,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Pr
1 (bases 1 to 204371)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACU26357 204371 bp DNA HTG 08-JAN-2001
HTG 08-JAN-2001
HTG 08-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC026357.22 GI:12044426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC026357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 204371)
Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204371 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tamerisa, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vinson, R.,
```

```
Db 158350 ATTGAGGATGTCAGCAGGGAGTTTGTGGAGGAGTTCATCTGGCCCAGCCATCCAGTTCAGC 158291
                                                                                                 Db 158409 AAGGAAGATTTCAAGGAAAACCAGGAAGAA-GCATTGAAGCTTTGGGGGCCAAAAAGGTGTTC
                                                                                                                                                                                             Db 158469 CTCCTGTAGCTGAAGGAACAAGGCTATGATGTCATTGCCTACCTGGCCAACATTAGCCAG 158410
                                                                                                                                                                                                                                                                                           Db 158529 ATGTCCAGAAAAAGCTCTGTGGTTCTGGCCTACAGTGGTGGCCTGGACACCTCCTGCATC 158470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                               Matches 1145;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                      121 aaggaagacttcgaggaagccaggaaggaaggcactgaagcttggggccaaaaaggtgttc 180
                                                                                                                                                                                                                 61 ctcgtgtgggctgaaggaacaaggctattgacgtcattgcctatctggccaacattggccag.120
                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                       1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 8 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64581 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemistry: Dye-primer Bodipy: 6% of reads
Chemistry: Dye-terminator Big Dye: 94% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 201671 bases at least 040
Consensus quality: 204577 bases at least 030
Consensus quality: 205669 bases at least 030
Estimated insert size: 201838; sum-of-contigs estimation
Quality coverage: 9.7x in 020 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201958
202058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165049
191728
191828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101849
101949
134386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: RP11-85503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; L08821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP11-85503"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39919 с
                                                                                                                                                                                                                                                                                                                                                                                                                 85.2%;
92.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .204371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204371:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101848:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191827:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101948:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38928 g 60229 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 52254 bp in length gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of unknown length contig of 26679 bp in length gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of unknown length contig of 10130 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of unknown length contig of 1153 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown length contig of 30463 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of unknown length contig of 32437 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of unknown length contig of 49494 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                              Score 1055.4; DB 2; Length 204371; Pred. No. 2.1e-209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Information
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
                                                                                                                                                                                                                                                                                                                                                                                            8;
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                              158351
                                                                                                                                                                                                                                                                                                                                                                                          ω
```

Qy

밁 Q

Louis

Louis,

```
DEFINITION
                                   AC005000
                    Locus
                                                                                                                                                                                                                                                                                                                                                                                                  157577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157876 GACATTCTCGAGATTGAGTT-AAAAAAGGGGTCCCCGTGAAGGTGACTGACATCAAGGAT 157818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157930
                                                                                                                                                                                                                                                                                                                               157517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                                                                        961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccggtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCATTGCTCCCTGGAGCATGCCTGAGTTCTACAACCGGTTCAAGGGCCCACAACGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACAAGTGGAAATTGCCCACCGGGAGGGGGCCAAGTATGTCCCCATGGCGTCACGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aaggggaacgatcaggtccggtttgagctcagctgctactcactggcccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgcccacagga
                                                                                                                                                                                                  ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag 1200
                                                                                                                                                                                                                                                                          ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTCCACCTACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAA 157758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggcaccacccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGGGAGCGATCAGGTCCAGTTTGAGCTCAACTGCTACTCGCTGGCTCCCCAGATAAAG
                                                                                                           gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                         CTCGGCCGGTAGTCCCCACTGTCTCTCTACAATGAAAAGCTGGTGAGCGTGAACATGCAG
                                                                                                                                                                                                                                                                                                                               TCCCAGGAGCCAGTGGAAGGGAAAGTGCAGGTGTCTTCTTCAAGGGCCCAGGTGTACATC
                                                                                                                                                                                                                                                                                                                                                 gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACGGCGTGGGCCGTACTGACATCGTGGAGAACCGCTTTATTGGAATGAAGTCTCGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGAATACGCAAAGCACCACGGGATTCCCATCCTGGTCACTCCCAAGAACCTGTGGAGC
                                                                                                                                                                                   GGTGATTATGAGCCAATTGATGCTACTGGTTTCATCAACATCAGTTCCCTCAGGCTGAAG
AC005000 107314 bp DNA
Homo sapiens clone RP1-241P17,
 complete sequence
                      10-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158231
                                                                                                                                                                                                                                                                                                                                                                                                        157518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE CO
                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                  Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
 Ş
                                       밁
                                                                       Qy
                                                                                                             Вb
                                                                                                                                               Qy
                                                                                                                                                                                   В
                                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                                           DЬ
                                                                                                                                                                                                                                                                                                                                  DЬ
                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 1136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                       33500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33260 ArgrecageAAAGGCTCTGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCCTGCATC 33319
                                                                                                                                                                                                                                                            33440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                         121 aaggaagacttcgaggaagccaggaaggaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                           61 ctcgtgtgggttgaaggaacaaggctattgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                                                                aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                        gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
 ggtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacct
                                       AAGGGAAATGATCAGGTCCAGTTTGAGCTAAACTGCTACTCTCTGGCCCCCCCAGATAAA
                                                        aaggggaacgatcaggtccggtttgagctcagctgctactcactgg-ccccccagataaa 419
                                                                                                               GCACTGTATGAGGACCACTACCTCCTGGGCACCTCTCTCACCAGGCCCTGCATCGCCCGA
                                                                                                                                                                                                                                                                                                                                  AAGGAAGACTTTGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGGGGGCAAAAAGGTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                        CTCGTGTTACTGAAGGAACAAGGCTATGACATCATTGCCTACGTGGCCAACACTGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Aug 19, 2000 this sequence version replaced gi:3212991. Center project name: H_DJ241P17.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 (bases 1 to 107314)
Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (19-AUG-2000) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (bases 1 to 107314) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 107314)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC005000
AC005000.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 107314)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a 23911 c 23826 g 29845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .107314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP1-241P17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:9857564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.0%;
91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 8e-209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing Center, Washington 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                        33559
                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                   33619
                                                                                                                                                     360
                                                                                                                                                                                                                                                                                                                                    33439
                                           33679
                                                                                                                                                                                                                                                              33499
                                                                                                                                                                                                                                                                                                                                                                                                            33379
```

Ņ

밁 Qy В

Qγ д δÃ 밁 Q 밁 οy 밁 Q

Ş В Вр Qy Вþ Q 밁 γQ Дb Qγ Вb δÃ В δã Вþ Q 밁

Qy

```
HUMAS3PS
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                                                                                                                                                                  Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ρy
                                                                                                                                                SOURCE
                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                       TITLE
                                                                                                                              ORGANISM
     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                    34399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      540
                                                                                                                                                                                                                                                                                                                                                          cctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgca
                                                                                                                                                                                                                                                                                                                                           GGAATATCATCATCTCCAGAGCAAGGTCACTGCCAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                 GGTTGATTATGAGCCAATCGATGCCACCAGTTTCATCAACATCAATTCCCTCAGGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                999tgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaa 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTAGGCCAGGAGT-CCCTCTGTTTATCTACAACGAGGAGCTGGTGAGCATGAACGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACCATGGACCGGGAAGTATGCAAAATCAAATAAGGCCTGGGCTTGAAATTTGCTGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATCTATGAGACCCCAGCAGACACCATCGTTTACCATGCTCATTTAGACATCAGGGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCCCAGGAGTGAGTGGAAAGTGCAGGTGTCCGTCTTCAAGGGCCTGGTGTACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTGTATACCGGTTTCTGGCACAGCCTTGAGTGTAAATTTGTCCACCACTGCATTGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caccatggaccgggaagtgcgcaaaatcaaaccaaggcctgggcttgaaatttgctgagct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tggcaccaccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaa 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tatctacgagaccccagcaggcaccatcctttaccatgctcatttagaccatcgaggcctt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTACAGCTTGGGCCGTATTGACATCAAGGAGAACCACTTCACTGGAATGAAGTCCCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcatggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGACATTCTCGAGATCGAGTTCAAATAAGGAGTCCCCATGAAAGTGACCAACGTCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tgacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAAGCATTTCCAGGTCTCCCACGAAGACCCCAGGACCCGGCCAAAGCCCCCAGAACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATGGACGAGAACCTCATGCAGATCAGCAATGAGGCTGGAATCTTGGAGAACCCTAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    catggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATGGAACACAAAGCAACACGGGATTCCCATCCCAGTCACTCCCAAGAACCTGTGGAA 33799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gatggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggag 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTCATTGCTCCCTGGAGGATGCCCAAGTTCTACAACAGGTTCAAGGTCCGAAATGAÇCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular structures of human argininosuccinate synthetase pseudogenes. Evolutionary and mechanistic implications J. Biol. Chem. 259 (5), 3160-3166 (1984)
                                                    1 (bases 1 to 1868)
Freytag, S.O., Bock, H.G., Beaudet, A.L. and O'Brien, W.E.
                                                                                                                                                                             argininosuccinate synthetase;
                                                                                      Mammalia; Eutheria;
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                              Homo sapiens
                                                                                                                                                                 synthetase.
                                                                                                                                                                                                K01846.1 GI:179058
                                                                                                                                                                                                                                 Human argininosuccinate
                                                                                                                                                                                                                                                        HUMAS3PS
                                                                                                                                         Human genomic DNA, Charon-4A library of Lawn et al, clone psi-AS-3.
                                                                                                                                                                                                                                                      1868
                                                                                                                                                                                                                                                    dq
                                                                                      Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                 synthetase
                                                                                                                                                                           processed gene; pseudogene;
                                                                                                                                                                                                                                 pseudogene
                                                                                                                                                                                                                                                  31-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34159
```

```
DЬ
                                                               Qy
                                                                                                  В
                                                                                                                               δÃ
                                                                                                                                                                  В
                                                                                                                                                                                               Q
                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                               Qγ
                                                                                                                                                                                                                                                                                                Ъ
                                                                                                                                                                                                                                                                                                                             Qγ
                                                                                                                                                                                                                                                                                                                                                                 Дb
                                                                                                                                                                                                                                                                                                                                                                                               Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 1143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
   661
                                    861
                                                                                                  801
                                                                                                                                   541
                                                                                                                                                                  741
                                                                                                                                                                                                 481
                                                                                                                                                                                                                                  681
                                                                                                                                                                                                                                                               421
                                                                                                                                                                                                                                                                                                  621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   441
                                                                                                                                                                                                                                                                                                                                 361
                                                                                                                                                                                                                                                                                                                                                                   561
                                                                                                                                                                                                                                                                                                                                                                                                 301
                                                                                                                                                                                                                                                                                                                                                                                                                                 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctcgtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat 720
                                                                                                                 | atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacccccaagaac
                                                                                                                                                                                   atggagtacgcaaagcaacacgggattccccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                 9tcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
                                                                                                                                                                                                                                                                                                                                                                                                                                               gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCCTGCAGCTGAAGGAACAAGGCTATGATGTCATTGCCTACCTGGCCAACATTAGCCAG
                                                  | caagegeeteeaggtetetacaegaagaeeeaggaeeeageeaaageeeeeaaeaeeeeet
                                                                                                ATGAACAAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAATCCCAAGAAC
                                                                                                                                                                ATGGAATACGCAAAGCACCACGGGATTCCCATCCTGGTCACTCCCAAGAACCTGTGGAGC
                                                                                                                                                                                                                                GTCATTGCTCCCTGGAGCATGCCTGAGTTCTACAACCGGTTCAAGGGCCACAATGACCTG
                                                                                                                                                                                                                                                                                                                                                                                 aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                 GCACCGCATGAGGATCGCTACCTCCTGGGCACTTCTCTCACCAGGCCCTGCATCGCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aaggaagacttcgaggaagccaggaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                AAGGGGAGCGATCAGGTTTGAGCTCAACTGCTACTCGCTGGCTCCCCAGATAAAG
                                                                                                                                                                                                                                                                                                                                                                AAACAAGTGGAAATTGCCCACCGGGAGGGGGCCAAGTATGTCCCCATGGCGTCACGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGAAGATTTCAAGGAAACCAGGAAGAA-GCATTGAAGCTTGGGGGCCAAAAAAGGTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There is one expressed gene and 14 pseudogenes fo argininosuccinate synthetase in the human genome. Three of the pseudogenes (psi-AS-1, -3, -7) were sequenced, in addition to the cDNA (AS). The pseudogenes are 89-93% homologous to the cDNA and lack introns. The authors [1] estimate that psi-AS-1 and psi-AS-3 were created 10-11 million years ago (93% homology), and psi-AS-7 was created approximately 21 million years ago (89% homology). The functional gene contains 13 exons spanning 65 kb on chromosome 9 (9934-qter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84135824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ďď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 a 501 c 474 g upstream of a PstI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="ASSP3"
/note="G00-119-709"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="ASSP3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /map="9q11-q22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .1868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.9%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1052.2; DB 9 Pred. No. 2.2e-208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                 660
                                                                                                860
                                                                                                                                 600
                                                                                                                                                                800
                                                                                                                                                                                               540
                                                                                                                                                                                                                                                               480
                                                                                                                                                                                                                              740
                                                                                                                                                                                                                                                                                                680
                                                                                                                                                                                                                                                                                                                                                                620
                                                                                                                                                                                                                                                                                                                                                                                               360
                                                                                                                                                                                                                                                                                                                                                                                                                                560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
```

```
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
AC008717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACGGCGTGGGCCGTACTGACATCGTGGAGAACCGCTTTATTGGAATGAAGTCCCGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         catggcgtgggccgtattgacatcgttggagaaccgcttcattggaatggaagtcccgaggt 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTGATTATGAGCCAATTGATGCTACTGGTTTCATCAACATCAGTTCCCTCAGGCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         accatggaccgggaagtgcgcaaaatcaaaccaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCTAGGAGGCCCCGGCAGGCACCATCCTTTACCACGCTCATTTAGACATCAAGGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAATATCATCATCTCCAGAGCAAGGTCACTGCCAAATAG 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCGGCCGGTAGTCCCCACTGTCTCTCTACAATGAAAAGCTGGTGAGCGTGAACATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCATGGACTGGGAAGTGCACAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTG
                                                                                                                                            Center: Joint Genome Institute
                                                                                                                                                                                             Submitted (03-AUG-1999) Production Sequencing Facility, DOE Jo
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598,
                                                                                                                                                                                                                                               2 (bases 1 to 110716)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 110716)
DOE Joint Genome Institute.
                                                                                                                                                                              On Aug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC008717
Consensus quality: 99834 bases at least Q40
                 Summary Statistics
                                                 Center clone name: CIT978SKB_87B2
                                                                Center Project Name: 97638, H211
                                                                                Project Information
                                                                                                                Web site: http://www.jgi.doe.gov
                                                                                                                                Center Code: JGI
                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                AC008717.4 GI:9954578
                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                              Sequencing of Human Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 unordered pieces.
                                                                                                                                                                              31, 2000 this sequence version replaced gi:7454179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110716 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA HIG 23 CL. 2015. S clone CTB-87B2, WORKING DRAFT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1093
                                                                                                                                                                                                  Joint
98, USA
```

```
BASE COUNT
ORIGIN
                                                                                                                                                                                          Qy.
                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                          g
                                                  DЬ
                                                                                          QΥ
                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                        QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 1132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                          26518 ATGTCCAGCAAAGGCTCCATGGTTCTGGCCTACAGTGGTGGCCTGAACACCTCCTGCATC
                                                     26698
                                                                                                                                                                                                                                               26578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                               181
241 gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                      61 ctogtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                   1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                         ATTGAGGATGTCAGCAGGGAGTTTGTGGAGGAGTTCATCTGGGCGGCCATCCAGTCCAGC
                                                                                                                                                                                                                                             CTCGTGTGGCTGAAGGAACAAGGCTATGATGTCACTGCCTACCTGGCCAATACTGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 10596 bases at least Q30
Consensus quality: 106925 bases at least Q30
Estimated insert size: 155000; pulse field gel estimation
Estimated insert size: 199416; sum-of-contigs estimation
Quality coverage: 8.72 in Q20 bases; pulse field gel estimation
Quality coverage: 8.72 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            st as soon as it is available and the accession number will st be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8763
10762
129862
12938
13038
17628
17728
22088
22188
31160
31260
40250
40350
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1021
1121
3107
3207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6844
8663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4569
6744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="CalTech human BAC library 20313 c 20302 g 33775 t 1309 otl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .110716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="CTB-87B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54466: gap of unknown le
84335: contig of 28869 k
84435: gap of unknown le
110716: contig of 26281 k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110716:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22187: gap of (31159: cont.)g (9 ap of (40249: cont.)g (40349: gap of (40349: gap of (55366: cont.)g (55366: c
                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.3%;
91.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10761
10861
12937
13037
17627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1032; DB 2; Pred. No. 1.6e-204;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g of 8972 bp in length funknown length bf unknown length funknown length g of 15017 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
of 2076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
of 1819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
of 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown length
of 28869 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 4360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 4590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 2175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 1020 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by in length length by in length by in length length by in length length length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in l
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bp in length length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 110716;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            others
                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                  240
                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                  26637
                                                                                                                                                                                                                                                                                                                                               26577
                                                                                                                                                    26697
                                                       26757
                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
--
```

Š В οy Дb Qy Вb δÃ B QΥ 밁 QY Db δÃ В οy Вb Qy B В В Qy В ρy Ъ δÃ В QΥ Db δÃ Ър 80 Q 밁 26878 27178 27118 27058 26998 26938 27416 27298 27238 1076 656 596 536 421 776 716 956 ggagcatggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacccca 595 acctgatggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgt gtc----attgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatg aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacgggcgccacagga 360 agaaccaagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaaca 655 aggatggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgg 775 cccctgacattctcgagatcgagttcaaaaaaaggggtccctgtgaaggtgaccaacgtca AAAAAAGTGGAAACCGTCCAGCGGGTGGGGGCCCAAGTGTGTCCCCACACCCCCCACAAGA 26877 acatcctcggccgggagtccccactgtctctctacaatgaggagctggtggtggatgaacg CCCCTGACATTCTCAAGATCCAAATTCAAAAAAAGGGGTCCCCGTGAGGGTGACCAGCGTCA tgcagggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggc 1195 agctggtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcg TCTTCACCACAGACCGGGAAGTGCACAAAACCAATCAAGGCCTGGGCTTGAAATTTGCTG ccttcaccatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctg CCAAGTCCCAGGAGCCGGCAGAAGGGAAAGTGCAGGTGCCGGTCCTCAAGGGCCCAGGTGT AGCTGATATACACCAGTTTCTGACATAGCCCTGAGTGTGAATTTGTCCGCCCCTGCATCG 27759 1135 1015 895 835 715 27177 475 27535 27117 27057 535 26997 26937 26817 955 27415 27297 27237 27655 27595 27475 27355

Search completed: February 12, 2002, 13:53:21 Job time: 4134 sec

•			
		·	

```
Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
           Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-775-693-1
1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     930621 seqs, 428662619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    February 12,
:/SIDS2/gcgdata/geneseq/yeneseqn/NA1088.DAT:*

(SIDS2/gcgdata/geneseq/yeneseqn/NA1089.DAT:*

(SIDS2/gcgdata/geneseq/yeneseqn/NA1990.DAT:*

(SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT:*

(SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT:*

(SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:*

(SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:*

(SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:*

(SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT:*

(SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT:*

(SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*

(SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*

(SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*

(SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

(SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atgtccagcaaaggctccgt.....gcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqn/Na1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/Na1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/Na1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/Na1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/Na1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/Na1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/Na1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/Na1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/Na1987.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002, 12:42:27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search time 146.6 Seconds (without alignments) 7245.743 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1861242
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

เก
ӵ
3
z
2
2
-
ŝ

Result		% Ouerv			SOFFINALES	
No.	Score	Match	Match Length DB	DB	ID	Description
_	1232.6	99.5	1725	22	ААН72909	Human cervical can
2	1232.6	99.5	2810	22	AAH34821	Human colon cancer
w	1232.6	99.5	2812	21	AAF16219	
4	466.8	37.7	969	22	AAI12589	Probe #2522 for ge
5	466.8	37.7	969	22	AAI33937	Probe #2623 used t
6	466.8	37.7	969	22	AAI02494	Probe #2485 used t
7	450.4	36.4	678	22	AAI21777	Probe #11710 for q
80	450.4	36.4	678	22	AAI47060	
9	450.4	36.4	678	22	AAI07462	Probe #7453 used t
10	351.4	28.4	1048	21	AAF14080	Aspergillus oryzae
11	310.4	25.1	360	22	AAI28968	Colon tumour relat

New isolated nucleic acid for diagnosing and treating cervical cancer

a)	ი ი		a a	c	כ	o	၀ ၀	c	(0	O
44 44 45 44 45	38 40 10	35	3 3 3 3 3 2	30 31	28	25	23 24	21 22	19 20	17	15	12 13
40.4 40.4 39.4 39.4 4		41.8 40.6	50 50	56.4 56.2	96.4	134.6 134.6	134.6 134.6	156 1 4 3.8	166 158	204.6	227.2	278.6 229.2
	 			7.8 4.5	7.8	ა		12.6 11.6				22.5 18.5
2684 3052 588 1479 4707	2277 2277 2371	987 874 7542	92934 172325	3153 855 400	1100	1326 349980 127	1203 1209	250 259	175 269	1653 175	222	440 234
222	19 19 22	19 21 19	21 21	22 18 18	22	22 22	22 22	22 22	21 22	21	22	21
AAC3811/ AAH13926 AAF71221 AAH68245 AAX55560	AAV13836 AAV05372 AAF91874	AAV52348 AAF12057 AAV52191	AAA81473 AAF21613	AAH54077 AAV74785 AAV75150	AAH52904	AAF71920 AAH68528 AAY11829	AAH66511 AAH66512	AAH72308 AAH69430	AAZ80726 AAH71231	AAC34397 AAZ80429	AAC3024/ AAI29415	AAC98292 AAA70071
Human (PKO439) nucl Human (DNA sequenc Corynobacterium gl C glutamicum codin Viral-encoded sema	ຜ	Streptococcus pneu	ng s	S. epidermidis gen Staphylococcus aur Staphylococcus aur	. epidermidis	Corynebacterium gl C glutamicum codin		Human cervical can Human cervical can	Human colon cancer Human cervical can	Arabidopsis thalia Human colon cancer		

ALIGNMENTS

```
AAH72909
ID AAH7
RESULT
                                                                08-DEC-1999;
21-DEC-1999;
14-MAR-2000;
12-MAY-2000;
09-JUN-2000;
21-JUL-2000;
                WPI; 2001-375006/39.
                                                                                                                            08-DEC-2000; 2000WO-US33312
                                                                                                                                                             WO200142467-A2
                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                               Cervical cancer;
                                                                                                                                                                                                               Human cervical cancer marker nucleic acid 4183.
                                                                                                                                                                                                                                19-SEP-2001 (first entry)
                                                                                                                                                                                                                                                  AAH72909;
                                                                                                                                                                                                                                                                   AAH72909 standard;
                                                                                                                                             14-JUN-2001.
                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                ₽,
                                                                99US-0169681.
99US-0171350.
2000US-0189315.
2000US-0203791.
2000US-0210600.
2000US-0220114.
                                Deeds
                                                                                                                                                                                               cytostatic; pre-malignant condition; gene therapy; ss.
                                J,
                                                                                                                                                                                                                                                                   cDNA; 1725 BP
                                Berger
                                Ŋ,
                                 Zhao
```

```
Ş
                                                   Qy
                                                                            В
                                                                                                          Ωy
                                                                                                                                      В
                                                                                                                                                             Qy
                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                        망
                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                             망
                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ДЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                           Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Sin
Matches 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  progression of cervical cancer or a premalignant condition in a pand to select and/or assess the efficacy of a compound or therapy and the cervical cancer in a patient. The nucleic acids may almost the cervical cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for gene therapy.
                                                                                                                                                                                            672
 781
                                                                                  792
                                                                                                             661
                                                                                                                                        732
                                                                                                                                                                 601
                                                                                                                                                                                                                                               612
                                                                                                                                                                                                                                                                          481
                                                                                                                                                                                                                                                                                                       552
                                                                                                                                                                                                                                                                                                                                421
                                                                                                                                                                                                                                                                                                                                                           492
                                                                                                                                                                                                                                                                                                                                                                                     361
                                                                                                                                                                                                                                                                                                                                                                                                                432
                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312
                                                       721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   سر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                        ggcaccacccacagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                  caagegeetecaggtetetacaegaagaeeeaggaeeeageeeaageeeeeet
                                                                                                                                                                                                                                                            atggagtacgcaaagcacacgggattcccatcccggtcactccccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                            gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                      caagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccct
                                                                                                                                                                                           atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                         atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacccccaagaac
                                                                                                                                                                                                                                              atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                    gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                 gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                       aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                     aaggggaacgatcaggtccggtttgagctcagctgctactcactggcccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                           aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                        aaacaagtggaaatcgcccagcgggggggccaagtatgtgtcccacggcgcccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aaggaagacttcgaggaagccaggaaggaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aaggaagacttcgaggaagccaggaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctcgtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaaccattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           assessing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425 A; 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.5%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detecting compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1232.6;
No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Т;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating the cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acids may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  patient;
 840
                            911
                                                     780
                                                                                  851
                                                                                                                                                                                                                    600
                                                                                                                                                                                                                                               671
                                                                                                                                                                                                                                                                         540
                                                                                                                                                                                                                                                                                                     611
                                                                                                                                                                                                                                                                                                                                                                                                                                        360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
                                                                                                                                                                                           731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
```

```
RESULT
AAH34821
밁
                                                                                                                                                                                                                                                                                                                                                                                                                     δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                        дЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                      1332
                                                                                                                                                                                                                                                                                                                                                                                                                                         1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1152
                                                                                Nucleic acids encoding
                                                                                                                                                                   29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                    03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1021
                                                                                                                               Ruben
                                                                                                                                                                                                                 05-APR-2001.
                                                                                                                                                                                                                                  WO200122920-A2
                                                                                                                                                                                                                                                                      colorectal
                                                                                                                                                                                                                                                                                                                                                         AAH34821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1032
                                                                                                                                                (HUMA-) HUMAN GENOME
                                                                                                                                                                                              28-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                      1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    912
                                                                                                                                                                                                                                                                                                                                                                         N
                                                                                                    2001-235357/24.
DB; AAG75416.
                                                                                                                                                                                                                                                                                                                                                                                                             gaatatcatcgtctccagagcaaggtcactgccaaatag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaattttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                    gaatatcatcgtctccagagcaaggtcactgccaaatag
                                                                                                                                                                                                                                                                                                                                                                                                                                        ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tcccaggagcgagtggaaagtgcaggtgtccgtcctcaagggccaggtgtacatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                 colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coLon
                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                       preventing,
                                                                                                                                                                                                                                                                      carcinoma;
                                                                                                                               Barash
                                                                                                                                                                                                                                                                                                cancer antigen
                                                                                                                                                                                              2000WO-US26524
                                                                                                                                                                                                                                                                                cancer;
                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                  99US-0157137.
99US-0163280.
                                                                                                                              SC,
                                                                                                                                                                                                                                                                                                                                                        cDNA;
                                                                                                                                                SCI INC
                                                                                                                                                                                                                                                                               colon cancer antigen;
                                                                                                                                                                                                                                                                      SS
                                                                      4277 human
diagnosing
                                                                                                                               Birse
                                                                                                                                                                                                                                                                                                                                                        2810
                                                                                                                                                                                                                                                                                               encoding cDNA
                                                                                                                               Œ,
                                                                                                                                                                                                                                                                                                                                                        ₿P
                                                                                colon
                                                                        and/or
                                                                                                                               Rosen
                                                                        cancer-associated polypeptides,
r treating colorectal cancers -
                                                                       treating
                                                                                                                                                                                                                                                                                                SEQ ID
                                                                                                                                                                                                                                                                             diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                       1239
                                                                                                                                                                                                                                                                                                 NO:1903
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1200
                                                                                                                                                                                                                                                                                                                                                                                                                                         1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  900
```

AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention,

3414-3415;

9803pp;

English

```
Matches 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention.

N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
  1835
                                                                                                                                                                                                      1715
                                                                                                                                                                                                                                                                                                      1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1295 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                       421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aaggaagacttcgaggaagccaggaagacagccactgaagctttggggccaaaaaggtgttc
                    atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacccccaagaac
                                                                                                                       atggagtacgcaaagcacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                        gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                      aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                           aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgcccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctcgtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
atggatgagaacctcatgcacatcagctacgaggctggaatccttggagaacccccaagaac
                                                                                             atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                gicattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                              aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcactgtatgaggaccgctacctcctgggcacctctctttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aaggaagacttcgaggaagccaggaaggaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2810 BP; 594 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            767 C; 864 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1232.6;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      584 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence listing were sequences are present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                1834
                                                                                                                                                                                                1774
                                                                                                                                                                                                                                                                                                   1714
                                                                                                                                                                                                                                                                                                                                                                                                    1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1534
                                              600
                                                                                                                                                                                                                                                  480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
```

δÃ В δÃ 밁 QΥ 뫄 Qy Вp Qy Вb Qy В δÃ DЬ Qy 밁 Qy В Š В οy B QΥ B δÃ

밁

2015

ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat

gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat

780

disorders

such as

prostate cancer -

prostate agnosis of

201,

caagcgcctccaggtctctacacgaagacccaggacccaggccaaagcccccaacacccct

caagcgcctccaggtctctacacgaagacccaggacccagccaaagccccaacacccct

```
XXX A ACC XXX 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
AAF16219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
                                                      Prostate cancer associated gene sequences, referred cancer antigens, useful for treatment, prevention, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2135
                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                      (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2000; 2000WO-US05988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF16219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              781
                                                                                                                                                      2000-587513/55
DB; AAB57016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atctacgagaccccaggcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gaatatcatcgtctccagagcaaggtcactgccaaatag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              accatggaccgggaagtgcgcaaaatcaaaccaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atctacgagacccaggcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                               CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tcccaggagcgagtggaaagtgcaggtgtccgtcctcaagggccaggtgtacatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostate cancer antigen nucleotide sequence SEQ ID
                                                                                                                                                                                                                                                                                                            ROSEN
                                                                                                                                                                                                                                               Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                            C
                                                                                                                                                                                                                                                                                                                                      GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                      99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2533
                                                         d to as prosta
and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO:654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           960
```

```
dd
                                                                                                                                                 Ş
                                                                                                                                                                                       В
                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                Qy
   δã
                                        В
                                                                       δÕ
                                                                                                                                                                                                                                                               망
                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                рь
                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF15514 to AAB157303 represent sequences used in the exemplification of the present
                                                                                                                                                                                         1837
                                                                                                                                                                                                                                                                 1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to A/The prostate cancer antigens can have neuroprotective, cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1537
                                                                                                                1897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                             421
     721
                                                                                                                                                                                                                                                                                                                                                                                                                                                     361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atgtccagcaaaggctccgtggttctggcctacagtggcgtggcctggacacctcgtgcatc
ggcaccaccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                      gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                        gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                              caagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccct
                                                                                                                             caagcgcctccaggtctctacacgaagacccaggacccagccaaagccccaacacccct
                                                                                                                                                                                      atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                       atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacccccaagaac
                                                                                                                                                                                                                                                               atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaaccccgtggagc
                                                                                                                                                                                                                                                                                                atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                     gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                          gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                  aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgcccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gcactgtatgaggaccgctacctcctgggcacctctctttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gcactgtatgaggaccgctacctcctgggcacctctctttgccagggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaaggtgttc

        aaggaagacttcgaggaagccaggaaggaaggcactgaagcttggggccaaaaaggtgttc
        180

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctcgtgtgggtggaaggaacaaggctatgacgtcattgcctatctggccaaccattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                 Page 1093-1094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 594 A; 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1232.6;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to AAB57302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
```

```
RESULT
AAI125
DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΔÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вþ
                                                                                                                                                                                                                                                                                                                                                                                                12589
                                                                                                                                 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2017
                                                                                                            21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2137
                                                                                                                                                                                         30-JAN-2001; 2001WO-US00670
                                                                                                                                                                                                                                     WO200157278-A2
                                                                                                                                                                                                                                                                                cervical cancer;
                                                                                                                                                                                                                                                                                             Probe;
                                                                                                                                                                                                                                                                                                                 Probe #2522
                                                                                                                                                                                                                                                                                                                                        12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                   AAI12589 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2077
                                                                           (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      841
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gaatatcatcgtctccagagcaaggtcactgccaaatag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atctacgagaccccaggcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                         gaatatcatcgtctccagagcaaggtcactgccaaatag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                               2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tcccaggagcgagtggaaagtgcaggtgtccgtcctcaagggccaggtgtacatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                           human; microarray;
                                                                           MOLECULAR DYNAMICS
                                                                                               2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632368.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                    DK,
                                                                                                                                                                                                                                                                                                                 expression analysis
                                                                                                                                                                                                                                                                                           gene
                                                    Σ
                                                                                                                                                                                                                                                                                                                                                                                   ΒP
                                                                                                                                                                                                                                                                                           expression;
                                                      Rank
                                                                                                                                                                                                                                                                                                                in human cervical cell sample
                                                                                                                                                                                                                                                                                           cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         960
```

Human genome-derived

single

exon nucleic acid

cervical

epithelial

probes

useful

e for

gene expression

'n

```
RESULT
AAI33937
  XXX DXX AXX
                                                                                                                                                                               밁
                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                       рь
                                                                                                                                                                                                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            · Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SXCCCCCCCXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Ma
Best Loc
Matches
                                                                                                          AAI33937 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
 Probe; microarray;
                            Probe #2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                             917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from human HeLa cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SENP).
                                                                                                                                                                                                                                                             481
                                                                                                                                                                                                                                                                                                                  421
                                                                                                                                                                                                                                                                                                                                             741
                                                                                                                                                                                                                                                                                                                                                                                                  681
                                                                                                                                                                                                                                                                                                                                                                                                                                                        621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        441
                                                                                                                                                                                                                                                                                        797
                                                                                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rocar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match
                                                                                                                                     G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to human single exon nucleic acid
                                                                                                                                                                                       atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacc
                                                                                                                                                                         atggacgagaacctcatgtgtatcagctatgaggctggaatcctggagaaac
                                                                                                                                                                                                                                              atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                    9tCattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                        aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aaggaagacttcgaggaagccaggaaggcactgaagctttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                               atggaatacacaaagcaacatcggattcccatcccagtcactctcaagaacccgtggatc
                                                                                                                                                                                                                                                                                    glcattgctccctggaggatgcccgagttctactactggctcaatggctgcaatgatctg
                                                                                                                                                                                                                                                                                                                                       aaggagaacgatcaggtccagtttgagctcacctgct----cactggcccccagattaag
                                                                                                                                                                                                                                                                                                                                                                                             aaacaagtggaaattacccagcaggaggggcccaagtacgtatcctatggcatcatggga
                                                                                                                                                                                                                                                                                                                                                                                                          aaacaagtggaaatcgcccagcggagggggccaagtatgtgtcccacggcgcccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cttgtgtggctgaaggaacaaggacatgttgtcattgcctacctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atgtccagcaaaggatccatggttctggcccacagtggtggcctggacacctcctgcatg 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                  gccctgtatgaggactactacctcctgggcacctctctggctaggctctgcatcgcccac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aaggaagacttcgagaaagacaggaaggcatgcaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25; SEQ ID No 2522; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     969
                            used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
                            ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 A;
 human;
                                                                                                          DNA;
                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence is one such probe. The SENPs are derived is. The SENPs can be used to produce a single exon
                         measure gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.7%;
                                                                                                          969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255
 placenta;
                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 466.8; DB 22
Pred. No. 6.9e-114;
0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 G;
antenatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
 diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 969;
                                                                                                                                                                            968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes
                                                                                                                                                                                                                                 916
                                                                                                                                                                                                                                                                                                               480
                                                                                                                                                                                                                                                                                                                                                                    42C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                     856
                                                                                                                                                                                                                                                                                                                                          796
                                                                                                                                                                                                                                                                                                                                                                                                                                                    680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300
```

```
밁
                    Ωy
                                                             δÃ
                                                                                                        Qγ
                                                                                                                                                 Qy
                                                                                                                                                                                           Qy
                                                                                                                                                                                                                  Ъ
                                                                                                                                                                                                                                      QУ
                                          DЬ
                                                                                    Дb
                                                                                                                             DЬ
                                                                                                                                                                        В
                                                                                                                                                                                                                                                             Дb
                                                                                                                                                                                                                                                                                γQ
                                                                                                                                                                                                                                                                                                       Вþ
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying grexpression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic disorder;
 797
                      421
                                          741
                                                                361
                                                                                    681
                                                                                                         301
                                                                                                                              621
                                                                                                                                                   241
                                                                                                                                                                        561
                                                                                                                                                                                             181
                                                                                                                                                                                                                   501
                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                             441
                                                                                                                                                                                                                                                                                                       381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-)
                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
gtcattgctccctggaggatgcccgagttctactgctctactggctcaatggctgcaatgatctg
                                                                                                                                                                                                                                                                      gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                     aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                             gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                  aaggagaacgatcaggtccagtttgagctcacctgct----cactggcccccagattaag
                                                                                   aaacaagtggaaattacccagcaggagggcccaagtacgtatcctatggcatcatggga
                                                                                                                             gccctgtatgaggactactacctcctgggcacctctctggctaggctctgcatcgcccac
                                                                                                                                                                       aaggaagacttcgagaaagacaggaaggaaggcatgcaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                         cttgtgtggctgaaggaacaaggacatgttgtcattgcctacctggccaacattggccag
                                                                                                                                                                                                                                                                                                    atgtccagcaaaggatccatggttctggcccacagtggtggcctggacacctcctgcatg 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome-derived single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                     BP; 249 A; 255 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2623; 654pp; English
                                                                                                                                                                                                                                                                                                                                                           37.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Σį
                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                          Score 466
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                     244 G; 221 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank DR;
                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                           466.8;
No. 6.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              placenta
                                                                                                                                                                                                                                                                                                                                                          .9e-114;
                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                67;
                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probes useful
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                    Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                                                                                                               4.
                                                                                                                                                                                                                                                                                                                                                                                                                                    are
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SENP).
                                                                                                                                                                                                                                                                                120
 856
                     480
                                                              420
                                                                                                                                                                        620
                                                                                                                                                                                                                 560
                                                                                                                                                                                                                                      180
                                                                                   740
                                                                                                        360
                                                                                                                             680
                                                                                                                                                   300
                                                                                                                                                                                           240
                                         796
```

Ļ.

```
ARESULT ARADOLAY ARAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                         Query Match
Best Local
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                  The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prob hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI02494 standard; DNA; 969 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-2001
                                                                                                                                     Sequence 969
                                                                                                                                                                                                                    Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2001; 2001WO-US00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe #2485 used to measure gene expression in human breast sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481
                            Local Similarity
                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atggagtacgcaaagcaacacgggattcccattcccggtcactcccaagaaccccgtggagc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-476286/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacc 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atggacgagaacctcatgtgtatcagctatgaggctggaatcctggagaaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atggaatacacaaagcaacatcggattcccatcccagtcactctcaagaacccgtggatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single exon nucleic acid human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID No 2485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0180312
2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-0234685
2000US-02346359
2000US-0024263
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; breast disease; breast cancer; developedisease; proliferative breast disease;
                                                                                                                                        BP; 249 A;
                            37.7%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen
                                                                                                                                        255 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ę
  0;
                            Score 466.8; DB 22
Pred. No. 6.9e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probe used to measuring
                                                                                                                                     244 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank
Mismatches
                                                                                                                                        221 T; 0 other;
                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              development
  67;
  Indels
                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-carcinoma tumour
                                                                                                                                                                                                                    part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorder;
                                                        969;
  4.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS
     <u>ب</u>
```

δÃ

atgtccagcamaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60

WPI;

2001-488901/53

```
RESULT

AAIIIT

AAIIIT

AC AAII

AC AAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                   04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
30-AUG-2000;
21-SEP-2000;
                                                      Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI21777;
                                                                                                        (MOLE-)
                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe; human; microarray; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe #11710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI21777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacc 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 cttgtgtggctgaaggaacaaggacatgttgtcattgcctacctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 atgtccagcaaaggatccatggttctggcccacagtggtggcctggacacctcctgcatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aaggaagacttcgagaaagacaggaagaaggcatgcaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | aaggaagacttcgaggaagccaggaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                      SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atggacgagaacctcatgtgtatcagctatgaggctggaatcctggagaaac 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atggaatacacaaagcaacatcggattcccatcccagtcactctcaagaacccgtggatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gtcattgctccctggaggatgcccgagttctactactggctcaatggctgcaatgatctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaggagaacgatcaggtccagtttgagctcacctgct----cactggcccccagattaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaacaagtggaaattacccagcaggaggggcccaagtacgtatcctatggcatcatggga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gccctgtatgaggactactacctcctgggcacctctctggctaggctctgcatcgcccac
                                                                                                        MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                      Hanzel DK,
                                                                                                                                                    2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                             2001WO-US00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for gene expression analysis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                         Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               678
                                                         Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression;
                                                         Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human cervical cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        796
```

```
RESULT
AAI47060
ID AAI4
XX
AC AAI4
XX
AC AAI4
XX
AT 17-C
XX
                                                                                                                                                  В
                                                                                                                                                                           20
                                                                                                                                                                                                        B
                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                    DЬ
                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                             DЪ
                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the prin specification, but was obtained in electronic format directly from WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing gene
                                                                          AAI47060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
               17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 678 BP; 168 A; 180 C; 182 G; 148 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SENP).
                                                                                                                                                                                                            585
                                                                                                                                                                                                                                         481
                                                                                                                                                                                                                                                                       525
                                                                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                                                                                                                                                469
                                                                                                                                                                                                                                                                                                                                                                                            409
                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                                    349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109
                                                                                                                                                                                                                                                                                                                                                           361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                     æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                atggatgagaacctcatgcacatcagctacgagg 574
                                                                                                                                                                                                                      atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                   gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                             aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                       amacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggggcccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                atggacgagaacctcatgtgtatcagctatgagg
                                                                                                                                                                                                          atggaatacacaaagcaacatcggattcccatcccagtcactctcaagaacccgtggatc
                                                                                                                                                                                                                                                                  gtcattgctccctggaggatgcccgagttctactactggctcaatggctgcaatgatctg
                                                                                                                                                                                                                                                                                                                             aaggagaacgatcaggtccagtttgagctcacctgct----cactggcccccagattaag
                                                                                                                                                                                                                                                                                                                                                                                         aaacaagtggaaattacccagcaggagggcccaagtacgtatcctatggcatcatggga
                                                                                                                                                                                                                                                                                                                                                                                                                                                  gccctgtatgaggactactacctcctgggcacctctctggctaggctctgcatcgcccac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaggaagacttcgagaaagacaggaaggaaggcatgcaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cttgtgtggctgaaggaacaaggacatgttgtcattgcctacctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atgtccagcaaaggatccatggttctggcccacagtggtggcctggacacctcctgcatg 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome-derived single exon nucleic acid probes useful for
zing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The
                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to human single exon nucleic acid present sequence is one such probe. The SENPs are depresent sequence is one such probe.
               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No 11710; 487pp; English
                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.4%;
87.8%;
                                                                         678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 450.4; DB 22; Pred. No. 1.3e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       printed
                                                                                                                                                                                                                                      540
                                                                                                                                                                                                                                                                                                 48C
                                                                                                                                                                                                                                                                                                                                                                                         468
                                                                                                                                                                                                                                                                                                                                                                                                                      360
                                                                                                                                                                                                                                                                                                                                                                                                                                                    408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                          644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲.
```

```
Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes The present sequence is one such probe. The probes are useful from producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes at for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe #15746 used to measure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 678 BP; 168 A; 180 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
 469
                                                                   409
                                                                                                    301
                                                                                                                                         349
                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                    169
                                                                                                                                                                                                                                                                                                                                                                                                                          109
                                  361
                                                                                                                                                                                                             289
                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                      aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgcccacagga
                                                                                                                                                                                                                               aaggaagacttcgaggaagccaggaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                   ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
              aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                         gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                           aaggaagacttcgagaaagacaggaaggaaggcatgcaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                   cttgtgtggctgaaggaacaaggacatgttgtcattgcctacctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                      atgtccagcaaaggatccatggttctggcccacagtggtggcctggacacctcctgcatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-488897/53.
aaggagaacgatcaggtccagtttgagctcacctgct----cactggcccccagattaag
                                                                   aaacaagtggaaattacccagcaggaggggcccaagtacgtatcctatggcatcatggga
                                                                                                                                       gccctgtatgaggactactacctcctgggcacctctctggctaggctctgcatcgcccac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome-derived single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0207456.

2000US-0608408.

2000US-0632366.

2000US-0234687.

2000US-02346359.

2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15746; 654pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 450.4; DB 22; Pred. No. 1.3e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 G; 148 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antenatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probes (SENP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                    420
                                                                                                      360
                                                                                                                                                                                                                                                                                                                                                    228
 524
                                                                                                                                         408
                                                                                                                                                                                                             348
                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                  288
                                                                                                                                                                                                                                                                                                                   180
```

1;

```
ARESULT AND ATTER AND ATTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ωy
                   Query Match
Best Local S
   Matches 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                             The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probabilities at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and
                                                                                            Sequence
                                                                                                                                               specification,
                                                                                                                                                                     Note:
                                                                                                                                                                                  non-carcinoma tumours
                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                Novel single exon nucleic acid in a human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe; human; breast disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe #7453 used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI07462 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481
                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                              human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atggaatacacaaagcaacatcggattcccatcccagtcactctcaagaacccgtggatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gtcattgctccctggaggatgcccgagttctactactggctcaatggctgcaatgatctg
                                                                                                                                              The sequence data for this patent did not form fication, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                      25; SEQ ID No 7453; 322pp; English.
                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULAR DYNAMICS
                                                                                            678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                            В₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                            168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 measure
                 36.4%;
                                                                                            ۸,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen
                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥,
                                                                                            c;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΒP
                 Score 450.4;
Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              breast cancer; development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                           probe used
                                                                                            182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank DR;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression
                                                                                          ç;
                                                                                            148 T;
                     1.3e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         678
                                                                                                                                                                                                                                                                                                                                                                                                                                           to measuring
                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in human breast sample
                                                                                            0
                                    22;
                                                                                            other
 Indels
                                    Length
                                                                                                                                               part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                      678;
                                                                                                                                                                                                                                                                                                               where the probe
 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                           expression
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480
1:
 Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ър
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ър
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
```

```
AAF14080
                                                                                                                                                                                                                                             Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis;
OVON (OVON)
                                                    22-MAR-1999;
                                                                                       22-MAR-2000;
                                                                                                                         28-SEP-2000
                                                                                                                                                           W0200056762-A2
                                                                                                                                                                                            Aspergillus oryzae
                                                                                                                                                                                                                               metabolic
                                                                                                                                                                                                                                                                                                                                Aspergillus
                                                                                                                                                                                                                                                                                                                                                                     13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF14080 standard; cDNA; 1048 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541 atggatgagaacctcatgcacatcagctacgagg 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aaggaagacttcgaggaagccaggaagacagcactgaagctttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atggacgagaacctcatgtgtatcagctatgagg 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atggaatacacaaagcaacatcggattcccatcccagtcactctcaagaacccgtggatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gtcattgctccctggaggatgcccgagttctactactggctcaatggctgcaatgatctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaggagaacgatcaggtccagtttgagctcacctgct----cactggcccccagattaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aaggggaacgatcaggtccggtttgagctcagctgctactcactggcccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aaacaagtggaaattacccagcaggaggggcccaagtacgtatcctatggcatcatggga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgcccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aaggaagacttcgagaaagacaggaaggaaggcatgcaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctcgtgtgggctgaaggaacaaggctattgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atgtccagcaaaggatccatggttctggcccacagtggtggcctggacacctcctgcatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cttgtgtggctgaaggaacaaggacatgttgtcattgcctacctggccaacattggccag
                                                                                                                                                                                                                             pathway engineering;
                                                                                                                                                                                                                                                                                                                                oryzae EST SEQ ID NO:6603
 NORDISK BIOTECH NORDISK AS.
                                                                                       2000WO-US07781
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                      99US-0273623
                   INC
                                                                                                                                                                                                                             catabolic
                                                                                                                                                                                                                             pathway engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
```

Berka RM,

Rey

Œ,

Shuster

JR,

Kauppinen

ß

Clausen

IG,

Olsen PB;

```
S
                                                       밁
                                                                                              Ş
                                                                                                                                               В
                                                                                                                                                                                      20
                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                            Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Aspergillus pryzae; and Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF14878 represents ESTs from Trichoderma reesei, which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in a first filamentous fungal (FF) cell relative to expression of genes same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown coan reading from the production of the microorganisms to be improved. New genes may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes are used in the methods for monitoring differential expression of genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1048 BP; 196 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        all specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     substrate of expressed sequence tags -
         499
                                                                                                                                                                                                                                           388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148
                                                                                                                                                                                                                                                                                                                                     328
                                                                                                                                                                                                                                                                                                                                                                                    259
                                                                                                                                                                                                                                                                                                                                                                                                                               268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
cacgggattcccatcccggtcactcccaagaacccgtggagcatggatgagaacctcatg
                                                                        atgcctgaattctacaaccggttcaagggccgcaatgacctgatggagtacgcaaagcaa 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gtggttctggcctacagtggcggcctggacacctcgtgcatcctcgtgtggctgaaggaa 78
                                                   gatcccaagttcttcaagcgtttcgctggccgtaacgatctcctcgactatgccgcccag
                                                                                                                                          cgtttcgaactggctttctatgccatccagccctccatcaagatcatcgccccttggcgt 507
                                                                                                                                                                     cggtttgagctcagctgctactcactggccccccagataaaggtcattgctccctggagg
                                                                                                                                                                                                                                    cagcgtgaaggctgccagtttgtcagccacggtgctaccggcaagggtaacgaccaggtc
                                                                                                                                                                                                                                                            cagcgggagggccaagtatgtgtcccacggcgccacaggaaaggggaacgatcaggtc
                                                                                                                                                                                                                                                                                                                                 tacctcctgggaaccagcttggctcgtcccgttatcgcccgcgcccagatgcgtgtcgct
                                                                                                                                                                                                                                                                                                                                                         tacctcctgggcacctctctttgccaggccctgcatcgcccgcaaacaagtggaaatcgcc
                                                                                                                                                                                                                                                                                                                                                                                                                           gagttcgtcgaggagctctgcttccctgccatccagtgcaatgccatctatgagggtcgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                gagtttgtggaggagttcatctggccggccatccagtccagcgcactgtattgaggaccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gttgaggagaaggccctcaagatcggtgccaagaagatggtgattgaggatctgcgccgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gccaggaagaaggcactgaagcttggggccaaaaaggtgttcattgaggatgtcagcagg 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gagggctacgaggttgtctgcttcctcggcaatgtcggccaggaggaagactgggccgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtctgtcttgcctactctggcggtctggataccagctgcattcttcgctggttgatcgag 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88; Page 2701; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention describes a method for monitoring differential of genes in a first filamentous fungal (FF) cell relative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 351.4; DB 2
Pred. No. 2.5e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 331; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 G; 237 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                       447
                                                                                                                                                                                                                                                                                                                                 387
                                                                                                                                                                                                                                                                                                                                                                               318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
```

```
RESULT :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DЬ
                                                                                                                                                                                         30-DEC-1999;
10-JAN-2000;
15-FEB-2000;
06-MAR-2000;
                                                                                            King
                                Colon tumor associated proteins and nucleic acids useful for prevention, diagnosis and treatment of colonic cancer -
                                                                                                                                                                  19-MAY-2000;
29-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                               Human; immunotherapy; diagnosis; colon cancer; colon tumour;
                                                                                                                                                                                                                                                                                                                                                                                     Colon tumour related determined cDNA sequence for contig
                                                                     WPI; 2001-441847/47
                                                                                                                                                                                                                                                     29-DEC-2000;
                                                                                                                                                                                                                                                                                                     W0200149716-A2
                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI28968 standard; cDNA; 360 BP
                                                                                                                                                                                                                                                                                                                                                   immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       982 cgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                919 cgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      922 atgaccatecteegegeegecatttegaeetegaaggtetegteetggaeggeeaggte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                568 accggcatccctgttacctccactaaggccaagccctggtccatggacgccaactccgcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggcaccatcctttaccatgctcatttagacatcgaggccttcaccatggaccgggaagtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gatattgtcgagaaccgcttcatcggtctcaagagccgtggctgctatgactcccctgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gacatcgtggagaaccgcttcattggaatgaagtcccgaggtatctacgaggaccccagca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tccttggagctcttcatgtacctgaacgaagtcgcgggcaagcatggcgtgggccgtatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tccgttgagctcttcaacgctctcaacaagctcggctacacccacggtgttggccgtatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttcgagcagggtatccccactaagct----cgtcactcccgagaagacatacaccgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tggaccatgaccgccgaccctctgaacgcccctaacgagcctgccgacatcaccatccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tacacgaagacccaggacccaacaagcccccaacacccctgacattctcgagatcgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cactgcagttacgaggccggtgttctggaggaccccaaccacacccctcccgctgacatg
          25; Page 273; 472pp; English
                                                                                          Lodes MJ,
E, Wang T,
                                                                                                                               CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         984
                                                                                                                                                                                         99US-0476296.
2000US-0480321.
2000US-0504629.
2000US-0519444.
                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                        2000US-0649811
                                                                                                                                                                  2000US-0575251
2000US-0609448
                                                                                                                                                                                                                                                     2000WO-US35596
                                                                                                       Secrist H,
                                                                                                                                                                                                                                                                                                                                                   therapy; vaccine; colonic cancer; ss
                                                                                            Jiang
                                                                                                        Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meagher MJ,
                                                                                                        Stolk JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    801
```

```
RESULT 1
AAC982 ID AAC982 ID AAC982 ID AAC982 ID AAC95 ID AAC95 XX ID IT O9-h
XX Huma
XX Inder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therefore which patients may be in need of restorative therapy. (1) may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. Anti-(1) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(1) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAI28460 to AAI29512 and AAM24494 to AAM24533 represent nucleotide and amino acid sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the polynucleotides (II) that encode them. (I) have cytostatic activity: (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP)
                         immunomodulatory; muscular; gynaecological; gastrointestinal;
nephrotropic; antiinfective; antibacterial; gene therapy; wound;
neural disorder; immune system disorder; muscular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                            AAC98292 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression, such as colonic cancer. For example, (I) and (II) may be
reproductive disorder; gastrointestinal disorder; renal disorder
                                                                                                                    identification; cytostatic; cardioactive; neuroprotective; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention describes colon tumour associated proteins (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acctgaacgaagtcgcgggcaagcatggcgtgggccgtattgacatcgtggagaaccgct 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tcctcaggggccaggtgtacctgmccgggcgg 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tcctcaagggccaggtgtacatcctcggccgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttgtccgccactgcatcgccaagtcccaggagcgagtggaaggggaaagtgcaggtgtccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctcatttagacatcgaggccttcaccatggaccgggaagtgcgcaaaatcaaacaaggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acctgaacgaagtcgcgggcaagcatggcgtgggccgtattgacatcgtggagaaccgct 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttgtccgccactacatcgccaagtcccaggagcgagtggaagggaaagtgcatgtgtccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgggcttgaaatttgctgagctggtgtataccggcttctggcacagccctgagtgtgaat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tgggcttgaaatttgctgagctggtgtataccggtttacggcctagccctgagtgtgaat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctcatttagacatcgaggccttcaccatggaccgggaagtgcacaaaatcmaacaaggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tcattggaatgaagtcccgaggtatctacgagaccccagcaggcaccatcctttaccatg
                                                                                                                                                                                                                   colon cancer antigen nucleotide sequence SEQ ID NO:302
                                                                                                                                                        colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    вP;
                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                               cDNA; 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; 96 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.1%;
95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 310.4;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2e-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
```

ρ рЬ 20 B Qy 밁 Qy 밁 Ş gg Ş

AAA70071/c ID AAA70071 standard; cDNA; 234

```
Ъ
                                                                    Дb
                                                                                                   QУ
                                                                                                                                         밁
                                                                                                                                                                           QУ
                                                                                                                                                                                                               В
                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, an can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB5407 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular,
                                                                                                      1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of co.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 738; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-2000; 2000WO-US05883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200055351-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infectious disease; cardiovascular disorder;
                                                                     189
                                                                                                                                                                                                                                                                                                    846 cgagaccccagcaggcaccatcctttaccatgctcatttagaccatcgaggccttcaccat 905
249
                                                                                                                                                                                                                 69
                                                                                                                                                                                                                                                                                   9
                                                                                                                                                          taccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaagtccca
                                                                                                                                                                                                                                ggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctggtgta
                                                                                    ggagcgagtggaagggaaagtgcaggtgtccgtcctcaagggccaggtgtacatcctcgg
                                 ccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgca
                                                                  ggagcgagtggaagggaaagtgcaggtgtccgtcctcaagggccaggtgtacatcctcgg
                                                                                                                                         taccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaagtccca
                                                                                                                                                                                                             ggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagntggtgta
                                                                                                                                                                                                                                                                                  cgagaccccagcaggcaccatcctttaccacgctcatttagacatcgaggccttcaccat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-587534/55.
ccgggagtccccactgtctctctacaatgaggagctggtgagcatggatgagaa
                                                                                                                                                                                                                                                                                                                                                         284;
            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     such as colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SM;
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                              116
                                                                                                                                                                                                                                                                                                                                                                        22.5%;
96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; 126 C;
                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                          Score 278.6;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                              115 G;
                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              78
                                                                                                                                                                                                                                                                                                                                                                      .2e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                         Length 440;
                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colon
                                                                                                        1085
                                                                                                                                                                                                                                                  965
                                                                                                                                                                                                                                                                                     83
                                                                                                                                           188
```

and

```
RESULT 14
AAC30247
                                                                           Qγ
                                                                                                       В
                                                                                                                                Qγ
                                                                                                                                                           В
                                                                                                                                                                                   Š
                                                   밁
                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-DEC-1998;
17-DEC-1998;
23-JUN-1999;
24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polynucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 18; Page 194; 299pp; English.
                                                                                                                                                                                                                                                                                                                                   Sequence 234 BP; 47 A; 63 C; 63 G; 61 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitcham JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200036107-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumour antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA70071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer, preferably ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ovarian carcinoma antigen polynucleotide
                                                                              842
                                                                                                       114
                                                                                                                                                            174
                                                                                                                                                                                                                                                                    Local Sin
hes 231;
                                                   54
                                                                                                                                                                                                                                                                                                                                                             resent human ovarian carcinoma polynucleotides and proteins used in exemplification of the present invention.
                                                TCTACGAGACCCCAGCAGGCACCATCCTTTACCACGCTCATTTAGACATCGAGG
                                                              tctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgagg
                                                                                                                                                       acattotogagatogagttoaaaaaaggggtocootgtgaaggtgaccaacgtoaaggatg 721
                                                                                                                 atggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggta
                                                                                                                                                                                                             ACATTCTGGAGATGGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-431589/37.
                                                                                                    ATGGCGTGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ovarian carcinoma; ovarian
                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          King GE,
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0216003.
99US-0338933.
99US-0404879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0215681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US30270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identification; cytostatic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                               18.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Algate
                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                              Score 229.2; DB Pred. No. 3e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PΑ,
                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frudakis
                                                                                                                                                                                                                                                                                             DВ
                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO:382
                                                                                                                                                                                                                                                                                            234;
                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                              Gaps
                                                                                                                               841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS.
                                                                                                                                                                                                                                                                 0;
```

ΧÏ

AAC30247 standard; cDNA;

RESULT 15 AAI29415/c ID AAI29415

standard;

CDNA;

222

```
멍
                                                                                       Qy
                                                                                                                       Ъ
                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                          Вþ
                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                               mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and foodiagnostic, forensic, gene therapy and chromosome mapping procedum
                                                                                                                                                                                                                                                                                                                         Sequence 270 BP; 59 A; 72 C; 83 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is one of a large number of 5' ESTs derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein 5' EST,
   220
                              181
                                                            160
                                                                                                                       100
                                                                                          121
                                                                                                                                                     61
                                                                                                                                                                                   40
                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                              1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
              aaggaagacttcgaggaagccaggaagacggcactgaagctttggggccaaaaaggtgttc
                                                                                                                                   ctcgtgtgggtgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
aaggaagacttcgaggaagccaggaaggaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                  ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcstscatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; SEQ ID 34322; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5' EST;
                                                                                                                                                                                                                                                                                                                                                       and secretion
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ļ
                                                                                                                                                                                                                                                           18.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence tag;
mapping; ss.
                                                                                                                                                                                                                                                                                                                                                       vectors.
                                                                                                                                                                                                                                            2:
                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO: 34322
                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                            No.
                                                                                                                                                                                                                                                                                                                         54 T; 2 other;
                                                                                                                                                                                                                                                                       227.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Giordano
                                                                                                                                                                                                                                                            1.1e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        secreted protein;
                                                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ų,
                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                         Length 270;
267
                            228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA isolation;
                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                            Gaps
                                                                                       180
                                                                                                                       159
                                                                                                                                                                                   99
```

0;

```
g
                                                                                                                                                                        Query Match
Best Local Similarity
                                                                            Matches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-DEC-1999; 99US-0476296.

10-JAN-2000; 2000US-04480321.

15-FEB-2000; 2000US-0504629.

06-MAR-2000; 2000US-0519444.

19-MAY-2000; 2000US-0579251.

29-JUN-2000; 2000US-0649811.
                                                                                                                                                                                                                                                                                                                                       produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vacciane production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to
                                                                                                                                                                                                                                                              and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xu J,
                                                                                                                                                                      Sequence 222 BP; 31 A; 49 C; 76 G; 66 T; 0 other;
                                                                                                                                                                                                                                 (e.g. by enzy and AAM24494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-441847/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-DEC-2000; 2000WO-US35596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200149716-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immunotherapy; diagnosis; colon cancer; colon tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Colon tumour related determined cDNA sequence for clone R0097:C02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI29415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogenic; gene therapy; vaccine; colonic cancer; ss.
by enzyme linked immunosorbant assay (ELISA)). AAI28460 to AAI29512
AM24494 to AAM24523 represent nucleotide and amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Page 400; 472pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lodes'MJ,
E, Wang T,
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                         exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secrist H,
, Jiang Y;
                                                                                            17.9%;
                                                                            0;
                                                                          Score 222; DB 22;
Pred. No. 2.4e-49;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Benson DR, Meagher MJ, Stolk JA;
                                                                                                             DB 22; Length 222;
                                                                            Indels
                                                                            0;
                                                                        Gaps
                                                                            0
```

```
QУ
DЬ
                             Qy
                                                                В
                                                                                                                                     Ъ
                                                                                                                                                                     Q
            626 agacccaggacccagccaaagcccccaacacccctgacattc 667
                                                                  102
                                                                                                                                       162 TTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCA
                                                                                                                                                                        506
42
                                                                                   gctacgaggctggaatcctggagaaccccaagaaccaagcgcctccaggtctctacacga
                                                                                                                                                      ttcccatcccggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatca 565
                                                                  GCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCTACACGA
AGACCCAGGACCCAGCCAAAGCCCCCAACACCCCCTGACATTC
                                                                                                      625
                                                                    43
                                                                                                                                       103
```

Search completed: February 12, 2002, 13:12:38 Job time: 1811 sec

•				
1				
			•	
		•		
	•			
	•			

```
Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM nucleic -
                                                                                                                                                                                                                                                                                                                                                                                              Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0\% Maximum Match 100\%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                         O
                                                                                                                                                                                                             10
11
12
                                                                                                                                                                                                                                                                                                                                                                                                                                                               pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                    seq length:
seq length:
 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued_Patents_NA:*
1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              February 12, 2002, 12:45:52; Search time 85.53 Seconds (without alignments) 3280.793 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-775-693-1
1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
 Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atgtccagcaaaggctccgt.....gcaaggtcactgccaaatag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000000000
              4 US-09-103-840A-2
4 US-09-328-111-513
4 US-09-328-111-810
1 US-08-676-967-5
2 US-09-098-487-5
2 US-09-098-487-5
3 US-09-181-706-1
4 US-09-459-666-1
4 US-09-221-298-66
1 US-09-221-298-66
1 US-09-251-715A-2
1 US-08-459-448A-2
2 US-08-459-448A-2
3 US-08-459-595A-4
3 US-09-053-549-3
3 US-09-053-549-3
3 US-09-053-549-3
3 US-09-165-042-2
1 US-08-761-258-8
                                                                                                                                                                                                                                                                                                                                                                                               IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          702406
Sequence 810, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 8, Appli
                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                               Sequence 513, A
Sequence 810, A
Sequence 5, App
Sequence 5, App
                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                         Appli
```

Db D	RES US	
	y-10	44444 00000000000000000000000000000000
5 2 2 5 9 5 9 6 9 6 9 9 9 9 9 9 9 9 9 9 9 9 9	1 1 2 CO 2	& & & & & & & & & & & & & & & & & & &
ge ge	AOA-2 APPL Control T: FLE T: VER T: VER T: VER T: VER TINVER INVER INVER INVER APPLIO APPLIO PELLIN FILIN FILIN FORM NEORM	ωωωωωνννννν» φοσοων
Col	Plic 4328 4328 EISC ERASE ERASE RASE RASE RASE RASE RASE RA	
Conserval cottggcctal	N: N: N: N: N: N: N: N: N: N: N: N: N: N	<i>~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~</i>
Conservative cotggcctacagtg	AN, Robe OWEN R. Claire John CC DA SEC TUBERR 1988 1988 2 1998 SS: 2 Ver. 2. Ver. 2. CCC 15 Ecrium t Ecrium t Ecrium t Ecrium t Ecrium t Ecrium t	2681 4014 1394 2938 2938 1358 1358 1358 1358 1358 1358 1358 13
yty	Cu obe 2 Seces and 3	
re 0; ttggcggcc	/09103840A bert D. e M. c M. COTONO OTONO OTONO R: US/09/1 8-06-24 8-06-24 1.1 1.1 1.1 1.1 2.1 3.2 3.2 3.3 3.48; Scol. 3.68; Pree	SSD SSD SSD SSD SSD SSD SSD SSD SSD SSD
gcotg ggtctcccctat cctat cctat ctgaag ctgaat ctatcd ctcatcd ctcatcd	into into into into into into into into	AF 088 088 088 088 088 088 088 088 088 08
Mismate	OR STHOOR STHOOR STHOOR STHOOR STHOOR STHOOR STHOOR STHOOR STANDARD STANDARD STREET STANDARD	-928 -541 -806 -969 -120 -121 -471 -471 -471 -470 -470 -083 -300 -083 -712 -083
Mismatches ggacacctcg tggacacctcg tggacacctcg tggcgatcga actgcggcgc gcctgccagcc ttgccaggccac	TRAI 340A pr g	-08-928-213B-7 -09-541-782-1 -08-806-263-1 -08-969-815-3 -09-120-025-3 -09-101-146-44 -08-471-034-45 -08-471-046A-4 -08-469-334-45 -08-393-785-14 -08-393-785-14 -08-393-948-13 -08-083-948-13 -08-083-948-13 -08-083-948-13
ches ctcgtc llll cctcgc caacat llll cctcgc ggccaa ggccaa ggccaa ll gcgcga	66 81	BAAAAA 1-11-13 1-145 1-145 1-145 1-145 1-145
542; ggtggc, ggtggc, attggc, attggc, attggc, attgg, alaaaa, cctcgg ggtgga,	NAL NAL	
Mismatches 542; In ggacacctcgtgcatcctcg tggacacctcggtggcatc tctggccaacattggccaga ttggcgatgacctcgggcag ttggcggccgacaacatggccg gcttgggcggcgacaacaaggtgt	t H	
Indels tcgtgtgg	S IN P	
	S IN MYCO	Sequence
Jb; (ctgaz)	ВаСТ! : the	uence luence
	5; s	11 12 13 14 14 14 15 16 17 17 17 17 17 17 17 17 17 17 17 17 17
ps 1867 134 134 1991 1991 1991 1991 1991 1991 1	equenc	Appli Appli Appli Appli Appli Appl Appl
4; 2308 2368 52428 52488	<u>^</u>	4444444444444444

```
Db 1863359 ccagtccgccgccgcggcttcgtctacgt 1863388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 1863299 cagcgcggaatcgttgtacgacttcaacctggccacctacgacgagggcgacagcttcga 1863358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-328-111-513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 1863179 gctgtggtactcgccgctgaaggccgcgctggaggctttcgtcgccaagacccaggagca 1863238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 1863119 tgagctgggccggttcaaacgccagaccgaccagcgctgggccgaactggtctacgacgg 1863178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 1863059 gcccggcgcgatggtgctgatcaccgcgcacaccgaactcgaacacgtcaccctggagcg 1863118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 1862999 gcgcctcgacgtcgtggaggatcggctggtgggcatcaagagccgcgagatctacgaggc 1863058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 1862939 ggtgtcgatgctggcggcgatcgaggagctcaaccgccgcgccggagcgcaaggtgtcgg 1862998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 1862894 cgtcggcttcgaacgcggcgtgccggtgtccgt------cgacggcaagcc 1862938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 1862834 ggacatctacgcctacaccgaagaccccacgatcaactgggggggtccccgacgaggtgat 1862893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 1862714 cgaggagaacgcgatcccgatcaacgtcaccaaacgttcgccgttctcccatcgaccagaa 1862773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 1862669 ggtgcg------cgactacgcgtggacgcgggagaaggcgatcgcgttcgc 1862713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 1862609 ccaggtccggttcgaagtcgggttcgcctcgctggcaccggatttagaggtgttggcgcc 1862668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 1862549 cgcggcgcgagcacggcgggcgtcgtcgtcgcgcacggctgcaccggcaagggcaacga 1862608
                                                                                                                                                                Sequence 513, Application US/09328111 Patent No. 6262333 GENERAL INFORMATION:
              APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: AStle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
                                                                                                                                                                                                                                                                                                                                                                                           1152 gccaactgatgccaccgggttcatcaacat 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1092 gtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcagggtgattatga 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       912 ggaagtgcgcaaaatcaaagacctgggcttgaaatttgctgagctggtgtataccgg 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              972 tttacggcctagcctgagtgtgaatttgtccgccactgcatcgccaagtcccaggagcg 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     852 occagoaggcaccatcctttaccatgctcatttagacatcgaggccttcaccatggaccg 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  792 ccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggtatctacgagac 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                732 ccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaagcatggcgtggg 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              672 gatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggatggcaccaccca 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            612 aggtototacacgaagacocaggacocagocoaaaggococaacacococtgacattotoga 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             552 cctcatgcacatcagctacgaggctggaatcctggagaaccccaagaaccaagcgcctcc 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492 aaagcaacacgggattcccatcccggtcactcccaagaacccgtggagcatggatgagaa 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 ctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctgatggagtacgc 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 tcaggtccggtttgagctcagctgctactcactggccccccagataaaggtcattgctcc 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 aatcgcccagcgggaggggccaagtatgttgtcccacggcgccacaggaaaggggaacga 371
```

```
APPLICANT: FORD, DONNA M.

APPLICANT: Lewis, Marcia E.

APPLICANT: Monahan, John E.

APPLICANT: Monahan, John E.

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS

FILE REFERENCE: CCD-257 (US)

CURRENT APPLICATION NUMBER: US/09/328,111

CURRENT FILING DATE: 1999-06-08

EARLIER APPLICATION NUMBER: US 60/088,801

EARLIER APPLICATION NUMBER: US 60/088,801

MUMBER OF SEQ ID NOS: 850

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 513

LENTH: 175
; ORGANISM: Homo sapiens US-09-328-111-810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-328-111-810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΩV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-09-328-111-513
                                                            SEQ ID NO 810
LENGTH: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 810, Application US/09328111 Patent No. 6262333
                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS FILE REFERENCE: CCD-257 (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 166; Conservative
                                                                                                                            NUMBER OF SEQ ID NOS: 850
                                                                                                                                        EARLIER APPLICATION NUMBER: US 60/088,801 EARLIER FILING DATE: 1998-06-10
                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                 APPLICANT: Lewis, Marcia E. APPLICANT: Monahan, John E. APPLICANT: Schlegel, Robert
                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bushnell, Steven E APPLICANT: Carroll III, Eddie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Steinmann, Kathleen E. APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Catino, Theodore J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Burgess, Christopher C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Endege, Wilson O.
                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Catino, Theodore J. APPLICANT: Derti, Adnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1194 getgaaggaatateategteteeagageaaggteaetgeeaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1134 cgtgcagggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcag 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 gctgaaggaatatcatcgtctccagagcaaggtcactgccaaatag 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 cgtgcagggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcag 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                     FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                      Derti,
                                                                                                                                                                                                                                                                                                                                                                    Ford, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Derti, Adnan
                                                                                                                                                                                                                                                                                                                                                                                         Adnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.4%; Score 166; DB 4; Length 175; 100.0%; Pred. No. 2.6e-40; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
```

0;

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-676-967-5
                                                                                                                                                                                                                                                                                               ; TOPOLOGY: li
; MOLECULE TYPE:
US-08-676-967-5
                                                                                                                                                                       Ş
   밁
                                 Ş
                                                                    В
                                                                                                   Š
                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08676967 Patent No. 5747317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                            Matches 122;
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1134 cgtgcagggtgattatgagccaactgatgccaccgggttcatcaacatcaacttccctcag 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1194 gctgaaggaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 gctgaaggaatatcatcgtctccagagcaaggtcactgccaaatag 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 cgtgcagggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcag 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 200 - CITY: San Francisco
                                                                                                                                      576 GGACAAGTACAAGGACACCCAGAGCGTGAGCGCCATCGGCGAGGAGAAGAGCCCACGAGAG 635
                                                                                                                                                                     516 ggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcagctacgaggc 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                     576 tggaatcctggagaaccccaagaaccaagcgcctccaggtctctacacgaagacccagga 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
696 GAACGACGACGACGACGACGACGACGACGACGCGCGTGTTCGACGACGACGACGA
                               636 cccagccaaagcccccaacacccctgacattctcgagatcgagttcaaaaaaaggggtccc 695
                                                                    636 CAAGCACCAGGAGAGCGTGAAGAAGAAGGCCCGCGAGGAGGAGGACATGGAGGAGGAGGA 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: UCB96-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/676,967
                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166;
                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osman Ph.D., Richard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                       2277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COLLINS, KATHLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science & Technology Law Group
                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                     cDNA
                                                                                                                                                                                                                                                                                                                                                      double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Telomerase
                                                                                                                                                                                                                             3.3%; Score 40.4; DB 1; Length 2277; 47.3%; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                  0; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pred. No. 2.6
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.6e-40;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                         0,
```

```
QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-676-974-5
                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                      В
                                                                                                                                                                                                                                     QY
                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-676-974-5
                                                                                                                                                                    Ωy
                                                                 B
                                                                                                Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08676974 Patent No. 5770422
밁
                             δÃ
                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: COLLINS, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   696 tgtgaaggtgaccaacgtcaaggatggcaccaccaaccagacctccttggagctcttcat 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                756 GGAGGAGGAGAACATCGAGAGCAAGGTGACCAAGCCCGTGCAGATCCAGAAGCGCGCCGT 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               816 GAAGCGCCCCCCCCCC 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              756 gtacctgaacgaagtcgc 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                        576 GGACAAGTACAAGGACACCCAGAGCGTGAGCGCCATCGGCGAGGAGAAGAGCCACGAGAG 635
                                                                                                                                                                                                                                                                                              516 ggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcagctacgaggc 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
                                                                                              696 tqtqaaqqtqaccaacgtcaaggatggcaccaccaccagacctccttggaqctcttcat 755
                                                                                                                                   696 GAACGACGACGACGACGACGACGACGACGAGGAGGACGCGTGTTCGACGACGAGGACGA 755
                                                                                                                                                                  636 cocaqccaaagcccccaacacccctgacattctcgagatcgagttcaaaaaaggggtccc 695
                                                                                                                                                                                                      636 CAAGCACCAGGAGAGGCGTGAAGAAGAAGGGCCGCGAGGAGGAGGACATGGAGGAGGAGGA 695
                                                                                                                                                                                                                                     576 tggaatcctggagaaccccaagaaccaagcgcctccaggtctctacacgaagacccagga 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
816 GAAGCGCCCCCCCCCCC 833
                                                               756 GGAGGAGGAGAACATCGAGAGCAAGGTGACCAAGCCCGTGCAGATCCAGAAGCGCGCCGT 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/676,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                               756 gtacctgaacgaagtcgc 773
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                               122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osman Ph.D., Richard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Science & Technology Law Group
268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (415)343-4342
(415)375 NO: 5:
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Telomerase
                                                                                                                                                                                                                                                                                                                                                                 3.3%;
47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KATHLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36,627
                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UCB96-055
                                                                                                                                                                                                                                                                                                                                                                 Score 40.4; DB 1; Length 2277; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                      136;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                          Gaps
```

```
; Sequence 1, Application US/09181706
; Patent No. 6130068
; GENERAL INFORMATION:
                                                          US-09-181-706-1
                                                                                 RESULT
                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                δ
δ
                                                                                                                                                                                                                                                                                   멍
                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: US-09-098-487-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-09-098-487-5
Sequence 5, Application US/09098487
Patent No. 5917025
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415)343-434
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                             816 GAAGCGCCCCGCCCCCCC 833
                                                                                                                                                                                         756 GGAGGAGGACATCGAGAGCAAGGTGACCAAGCCCGTGCAGATCCAGAAGCGCGCCGT 815
                                                                                                                                                                                                                 696 tgtgaaggtgaccaacgtcaaggatggcaccaccaccagacctccttggagctcttcat 755
                                                                                                                                                                                                                                                               696 GAACGACGACGACGACGACGACGACGAGGAGGACGGCGTGTTCGACGACGACGACGA
                                                                                                                                                                                                                                                                                                  636 cccagccaaagcccccaacacccctgacattctcgagatcgagttcaaaaaaggggtccc 695
                                                                                                                                                                                                                                                                                                                                                              576 tggaatcctggagaacccaagaaccaagcgcctccaggtctctacacgaagacccagga 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                756 gtacctgaacgaagtcgc 773
                                                                                                                                                                                                                                                                                                                                     636 CAAGCACCAGGAGAGCGTGAAGAAGAAGGCCCGCGAGGAGGAGGACATGGAGGAGGACGA 695
                                                                                                                                                                                                                                                                                                                                                                                                             576 GGACAAGTACAAGGACACCCAGAGCGTGAGCGCCATCGGCGAGGAGAAGAGCCCACGAGAG 635
                                                                                                                                                                                                                                                                                                                                                                                                                                  516 ggtcactcccaagaacccgtggagcatgggatgagaacctcatgcacatcagctacgaggc 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COLLINS, Kathleen
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/098,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Science & Technology Law Group
268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (415)343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.3%; Score 40.4; DB 2; Length 2277; 47.3%; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UCB96-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
```

0;

```
US-09-458-791-1
                                                                                                                                                                                 밁
                                                  RESULT
                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                       ₽
                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION:
US-09-181-706-1
Sequence 1, Application US/09458791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FRIGHH: 4707 base pairs
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                     743 ACTACCCCTACAACTATACGAGCGGCGCTGCCACCGGCTGGCCCAGCATGGCGCGCA 799
                                                                                                             245 tgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgccgca 301
                                                                                                                                                             683 GCGCGGGCAGCCTGCACTTCGTGGACGCCTTTCTCTGGAACGGCAGCATCTACTTCCCCT 742
                                                                                                                                                                                                                                      623 AGGACACGGAGGGGCAGCCTGGCCACGCAGGAGCTGGGGCCCCCCAAGCTGTGCGAGG 682
                                                                                                                                                                                                                                                             125 aagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttcattg 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (206)470-4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,5
                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
FILING DATE: October 26, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Melanie K. Spriggs, Michael R. Comeau, APPLICANT: Robert F. DuBose, Richard S. Johnson TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: Janis C. Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                      watch 3.2%; Score 39.4; DB 3; Length 4707; Local Similarity 51.4%; Pred. No. 0.091; ndels 0; Mismatches 86; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/958,598 (converted to a APPLICATION NUMBER: Provisional, see below) FILING DATE: October 28, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 51 Uni
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                     1..4707
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   October 28, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/09/181,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2631-A
                                                                                                                                                                                                                                                                                                                  86;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                          0; Gaps
```

NUMBER OF SEQUENCES:

```
밁
                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                        ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-458-791-1
                                                                                                                                US-09-459-066-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6174689
GENERAL INFORMATION:
GENERAL Spriggs, Melanie
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
Sequence 1, Application US/09459066
Patent No. 6.187909
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCOD
TITLE OF INVENTION: RECEPTOR DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4707 base pairs
                                                                                                                                                                                                                                         245 tgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgca 301
                                                                                                                                                                                                                                                                                                  683 GCGCGGGCAGCCTGCACTTCGTGGACGCCTTTCTCTGGAACGGCAGCATCTACTTCCCCT 742
                                                                                                                                                                                                                                                                                                                           623 AGGACACGGAGGGGCGCAGCCTGGCCACGCAGGAGCTGGGGGCGCCTCAAGCTGTGCGAGG 682
                                                                                                                                                                                                                                                                                                                                                                                                             125 aagacttcgaggaagccaggaaggaaggcactgaagcttggggccaaaaaaggtgttcattg 184
                                                                                                                                                                                                                743 ACTACCCCTACAACTATACGAGCGGCGCTGCCACCGGCTGGCCCAGCATGGCGCGCA 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS/Windows 95 SOFTWARE: Word for Windows 95, 7.0a CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/958,598 FILING DATE: 28-OCT-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
TELEPAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n 3.2%;
Similarity 51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/458,791 FILING DATE: 10-Dec-1999 CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Janis C. Henry STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..4707
                        Melanie
VIRAL ENCODED SEMAPHORIN PROTEIN
        RECEPTOR DNA AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR DNA AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39.4; DB 4; Length 4707; Pred. No. 0.091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-459-066-1
                                                                                                                                                                                                                US-09-103-840A-2/c
                                                                                                                                                                                                                                 RESULT
                                                                                                                                         ; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                             ; Sequence 2, Application US/09103840A ; Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
APPLICANT VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM FILE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UNUBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Word for Win
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS: ADDRESSEE: Janis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                        683 GCGCGGGCAGCCTGCACTTCGTGGACGCCTTTCTCTGGAACGGCAGCATCTACTTCCCCT 742
                                                                                                                                                                                                                                                                                                                                                                                      623 AGGACACGGAGGGGCGCAGCCTGGCCACGCAGGAGCTGGGGCCCTCAAGCTGTGCGAGG 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 aagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttcattg 184
                                                                                                                                                                                                                                                                                   743 ACTACCCCTACAACTATACGAGCGGCGCTGCCACCGGCTGGCCCAGCATGGCGCGCA 799
                                                                                                                                                                                                                                                                                                                 245 tgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgca 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Henry, Janis C
REGISTRATION NUMBER: 34.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS-DOS/Windows 95 SOFTWARE: Word for Windows 95, 7.0a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/459,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4707 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..4707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (206)470-4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.2%;
51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08/958,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39.4; DB 4; Length 4707; Pred. No. 0.091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
```

0;

```
US-07-951-715A-2
; Sequence 2, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       망
                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 1419599 TGGCCACCCAGCAAGCCCAGCTGGTCTGCAAGAAGCTGGCCAGCGGCGAAACCGGCACCG 1419540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-221-298-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-221-298-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 1419659 AAGACGAAGCCTTCATTGCTCAGATGGAGTCCATTGGCGTCACCTTCTCCTCACCGCAGG 1419600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: CDC 1551 , OTHER INFORMATION: "n" bases at various positions throughout the sequence ; OTHER INFORMATION: represent a, t, c or g US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GOMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER
TITLE OF INVENTION:
GOMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS
TITLE OF INVENTION:
GENERAL INFORMATION INFORMATION OF COLON 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 66, Application US/09221298 Patent No. 6284241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 204
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver.
       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                          168 caaaaaggtgttcattgaggatgtcagcagggagtttgtggaggag 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 ccaggaagaaggcactgaagcttggggccaaaaaggtgttcattgaggatgtcagcaggg 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 acctcctgggcacctctcttgccaggccctgcatcgcccgcaaac 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 agtitiqtggaggagttcatctggccggccatccagtccagcgcactgtatgaggaccgct 259
                                                                                                                                                                                                                                                                                86 ggaacagagcatctctgaagagcccggctgggaggaggaggaagag 131
                                                                                                                                                                                                                                                                                                                                                                                                                          26 ctataaagtccatcagttagagcaggagcaggccggagggacgccctgaagcagcgggc 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
Koziel, Michael G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.1%;
48.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37.2; DB 4; Length 204; Pred. No. 0.075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4403765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;;
```

```
; NAME/KEY: misc_feature
; LOCATION: 1.3468
; OTHER INFORMATION: /prod
; OTHER INFORMATION: optim
; OTHER INFORMATION: /note
US-07-951-715A-2
                                             γ
                                                                                                                                                  Query Match 3.0%;
Best Local Similarity 49.0%;
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: SPILLI, W. MUTTAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5-18
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8619
TELEPAX: (919)541-869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 2:
                            1060 ctcaagggccaggtqtacatcctcggccgggagtccccactgtctctctacaatgaggag 1119
                                                                                                       1000 gtccgccactgcatcgccaagtcccaggagcgagtggaagggaaagtgcaggtgtccgtc 1059
2545 GCCCTGGCCCGCGTGAAGCGCGCGAGAAGAAGTGGCGCGACAAGCGCGAGAAGCTGGAG 2604
                                                                         2485 GACGGCCACGCCCTGGGCAACCTGGAGTTCCTGGAGGAGAAGCCCCTGGTGGGCGAG 2544
                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Rela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: / STREET: / CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING INTELLIBRIC OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Cibh C. ADDRESSEE: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/951,715A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10532
                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3468 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.30B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pace, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dawson, John L.
Dunder, Erik M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bowman, Cindy G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rothstein, Steven J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Merlin, Ellis J.
Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wright, Martha S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Warren,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                   /product= "Full-length pure maize
optimized synthetic Bt"
/note= "Disclosed in Figure 3 as syn1T.mze"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYNTHETIC DNA SEQUENCE HAVING ENHANCED
                                                                                                                                                    0,
                                                                                                                                                Score 37.2; DB 1; Length 3468; Pred. No. 0.35; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S-18805/A/CGC 1577/CIP
                                                                                                                                                0;
                                                                                                                                              Gaps
```

0;

Ş

1120 ctggtgagcatgaacgtgcagggtgattatgagccaactgatgccaccgggttcatcaac 1179

```
Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-951-715A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           requence 4, Application US/07951715A Patent No. 5625136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                     TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1180 atcaattccctcaggctgaagg 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. MUTTBY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEPAX: (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING I
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2665 AGCCAGTACGACCGCCTGCAGG 2686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2605 TGGGAGACCAACATCGTGTACAAGGAGGCCAAGGAGAGCGTGGACGCCCTGTTCGTGAAC 2664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                        MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                        HYPOTHETICAL:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/951,715A FILING DATE: 25-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
 OTHER INFORMATION:
                                                                                                                              TOPOLOGY:
                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                    LOCATION:
                                  NAME/KEY: misc_feature
                                                                                                                                                                                 LENGTH:
                                                                                                                                                             nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dunder, Erik M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wright, Martha S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crossland, Lyle D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Warren, Gregory W. Evola, Stephen V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kramer, Vance C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desai, Nalini M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koziel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pace, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dawson, John L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merlin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bowman, Cindy G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lewis, Kelly S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rothstein, Steven J.
                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIBA-GEIGY Corporation
                                                                                        other nucleic acid
/desc = "Synthetic DNA"
                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ellis J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNTHETIC DNA SEQUENCE HAVING ENHANCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
/product= "Full length synthetic
```

```
DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-951-715A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-459-448A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08459448A Patent No. 5859336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1000 gtccgccactgcatcgccaagtcccaggagcgagtggaaggggaaagtgcaggtgtccgtc 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1060 ctcaagggccaggtgtacatcctcggccgggagtccccactgtctctctacaatgaggag 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2485 GACGGCCACGCCCGGCCAGCCAGCCTGGAGTTCCTGGAGGAGAAGCCCCCTGGTGGGCGAG 2544
                                CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/951,715
FILING DATE: 25-SEP-1992
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Suttie, Janet L. TITLE OF INVENTION: SYNTHET TITLE OF INVENTION: INSECTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2665 AGCCAGTACGACCGCCTGCAGG 2686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2605 TGGGAGACCAACATCGTGTACAAGGAGGCCAAGGAGAGCGTGGACGCCCTGTTCGTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1120 ctggtgagcatgaacgtgcagggtgattatgagccaactgatgccaccgggttcatcaac 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2545 GCCCTGGCCCGCGTGAAGCGCGCCGAGAAGAAGTGGCGCGACAAGCGCGAGAAGCTGGAG
                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                           APPLICATION NUMBER: FILING DATE: 02-JU
                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                         ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atcaattccctcaggctgaagg 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99;
                                                                                                                                                                                                                                                         10591-9005
                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Warren, Gregory W. Evola, Stephen V. Crossland, Lyle D. Wright, Martha S.
                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dawson, John L.
Dunder, Erik M.
Pace, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merlin, Ellis J.
Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kramer, Vance C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lewis, Kelly S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bowman, Cindy G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rothstein, Steven J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koziel,
                                                                                                           02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                          SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     maize optimized"
/note= "Disclosed in Figure 3 as synful.mod. This sequenc
identical to flsynbt.fin as disclosed in Figure 1."
 US 07/772,027
                                                                                                                            US/08/459,448A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37.2; DB 1; Pred. No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
```

ATTORNEY/AGENT INFORMATION:

FILING DATE:

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-459-448A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08459448A Patent No. 5859336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                            APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHET.
TITLE OF INVENTION: INSECTION
UNMER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1180 atcaattccctcaggctgaagg 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1060 ctcaagggccaggtgtacatcctcggccgggagtccccactgtctctctacaatgaggag 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1000 gtccgccactgcatcgccaagtcccaggagcgagtggaagggaaagtgcaggtgtccgtc 1059
                   CORRESPONDENCE ADDRESS
                                                                                                                      APPLICANT:
                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2665
                                                                                                                                         APPLICANT:
                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2485 GACGGCCACGCCCGGCCAACCTGGAGTTCCTGGAGGAGAAGCCCCTGGTGGGCGAG 2544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: 1.3468
OTHER INFORMATION: /proc
OTHER INFORMATION: /proc
OTHER INFORMATION: /note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 3468 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECÓMMUNICATION INFORMATION: TELEPHONE: (919)541-8582
                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Pace, Gary M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctggtgagcatgaacgtgcagggtgattatgagccaactgatgccaccgggttcatcaac 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGGAGACCAACATCGTGTACAAGGAGGCCCAAGGAGGCGTGGACGCCCTGTTCGTGAAC 2664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCTGGCCCGCGTGAAGCGCGCCGAGAAGAAGTGGCGCGACAAGCGCGAGAAGCTGGAG 2604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCCAGTACGACCGCCTGCAGG 2686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                    Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3468 base pairs
                                                                                                                                                                                          Launis, Karen L.
                                                                                                                                                                                                        Merlin,
                                                                                                                                                                                                                          Wright, Martha S.
                                                                                                                                                                                                                                            Crossland, Lyle D.
                                                                                                                                                                                                                                                                              Warren,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (919)541-8689
                                                                                                                                                                                                                                                                Evola,
                                                                                                                                                                                                                                                                                                                Lewis, Kelly S.
                                                                                                                                                                                                                                                                                                                                Desai, Nalini M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                  Koziel, Michael G.
   NO.
5859336artis Corporation
                                                                                                                                                                                                                                                            , Gregory W. Stephen V.
                                                                                                                                                                                                          Ellis J.
                                                                                                                                                                                                                                                                                                  Vance C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.0%;
                                                SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Full-length pure maize
optimized synthetic Bt"
/note= "Disclosed in Figure 3 as synlT.mze"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGC 1577/CIP/DIV4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37.2;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
```

```
Q
                                                                                                                                               밁
                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                               Ъ
                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-459-448A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.0%;
Best Local Similarity 49.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1000 gtccgccactgcatcgccaagtcccaggagcgagtggaagggaaagtgcaggtgtccgtc 1059
                                                                                                                                                                                     1120 ctggtgagcatgaacgtgcagggtgattatgagccaactgatgccaccgggttcatcaac 1179
                                                                                                                                                                                                                                                                                                                                                            1060 ctcaagggccaggtgtacatcctcggccgggagtccccactgtctctctacaatgaggag 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                       2485 GACGGCCACGCCCGGCCTGGGCAACCTGGAGTTCCTGGAGGAGAAGCCCCTGGTGGGCGAG
2665 AGCCAGTACGACCGCCTGCAGG
                                                                    1180 atcaattccctcaggctgaagg 1201
                                                                                                                                            2605 TGGGAGACCAACATCGTGTACAAGGAGGCCCAAGGAGAGCGTGGACGCCCTGTTCGTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US OF FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION: NAME: Pace, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/459,448A
                                                                                                                                                                                                                                                                                        2545 GCCCTGGCCCGCGTGAAGCGCGCCGAGAAGAAGTGGCGCGACAAGCGCGAGAAGCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: 1..3468
OTHER INFORMATION: /proc OTHER INFORMATION: /note OTHER INFORMATION: identification identification in the control of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 25-SEP-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10591-9005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent & Trademark Dept., 520 White Plains Rd., POB 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3468 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (919)541-8582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other nucleic acid
/desc = "Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Full length synthetic maize optimized" /product= "Disclosed in Figure 3 as synful.mod. This sequenc identical to flsynbt.fin as disclosed in Figure 1."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           us 07/772,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us 07/951,715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGC 1577/CIP/DIV4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37.2; DB Pred. No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                        2604
                                                                                                                                                                                                                                                                                                                                                                                                                                       2544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
```

Search completed: February 12, 2002, 14:41:32 Job time: 6940 sec

,				
÷	•		·	
		-		
		·		

```
Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM nucleic -
                                                                                                                                         No
   55
66
7
7
10
11
11
11
                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
  780.6
780.2
772.4
768.8
758.4
753.2
749.2
748.6
                                                                                  817.8
809.8
803.2
783
                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic search, using sw model
                                                                                                                                      Match Length
                                                                                                                                                                                                                                    Query
  66.0
65.4
64.8
63.2
63.0
63.0
63.0
62.3
62.3
62.1
61.2
60.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 atgtccagcaaaggctccgt.....gcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-775-693-1
1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            February 12, 2002, 12:41:27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                              em_estov:*
em_htc:*
                                                                                                                                                                                                                                                                                   gb_gss:*
em_gss_fun:*
em_gss_hum:*
em_gss_inv:*
                                                                                                                                                                                                                                                     em_gss_pln:*
em_gss_pro:*
em_gss_rod:*
                                                                                                                                                                                                                                                                                                                              gb_est1:*
gb_est2:*
gb_htc:*
                                                                                                                                                                                                                                                                                                                                                                                    em_estro:*
                                                                                                                                                                                                                                                                                                                                                                                              em_estba:*
                                                                                                                                                                                                                                                                                                                                                                                                        em_estom: *
em_estpl: *
                                                                                                                                                                                                                                                                                                                                                                                                                                        em_esthum:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                em_estfun:*
                                                                                                                                                                                                                                                                                                                                                                                                                              em_estin:*
                                                                                                                                                                                                                                   em_gss_other:*
                                                                                                                                                                                                                                             em_gss_vrt:*
878
878
838
875
815
980
905
918
918
952
881
1028
                                                                                                                                        DB
                                                                                                                                        IJ
                                                 BI256461
BI258834
BI256559
BI257913
BI260468
BE379161
BG828136
                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (without alignments)
9573.472 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search time 1390.72 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22703874
     BI256461 602974488
BI258834 60296964
BI256559 602976921
BI257913 602970844
BI2579161 6012363137
BE379161 601236323
BE379161 6012363939
BI085601 60287636363
BE379561 6012363939
BI085601 602879143
BE3706265 601869276
                                                                                                                                   Description
```

 $\begin{array}{c} 113 \\ 145 \\$

ALIGNMENTS

JOURNAL COMMENT FEATURES SOURCE ORGANISM RESULT BI256461 LOCUS ACCESSION VERSION REFERENCE KEYWORDS DEFINITION AUTHORS TITLE source Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 878)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC Plate: LLAM11276 row: o column: 22 High quality sequence stop: 835. Location/Qualifiers cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov BI256461 878 bp 602974488F1 NIH_MGC_12 Homo sapiens BI256461.1 GI:14810890 mRNA sequence. numan. /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGS:5113965"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B" 1. .878 Homo sapiens cDNA clone IMAGE:5113965 5', mRNA 17-JUL-2001 can

BI259920 BE378581 BI085601

```
ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          рь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                              망
                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                    Qγ
                                                                                                                                                                                                                                                                                    Дb
                                                                                                                                                                                                                                                                                                             Ωy
                                                                                                                                                                                                                                                                                                                                         Дb
                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                       망
                                                                               Ş
                                                                                                                                       δÃ
                                                                                                                                                                    망
                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145
                                                                                                               745
                                                                                                                                          719
                                                                                                                                                                       685
                                                                                                                                                                                                                              625
                                                                                                                                                                                                                                                         601
                                                                                                                                                                                                                                                                                                              541
                                                                                                                                                                                                                                                                                                                                            505
                                                                                                                                                                                                                                                                                                                                                                      481
                                                                                                                                                                                                                                                                                                                                                                                                  445
                                                                                                                                                                                                                                                                                                                                                                                                                           421
                                                                                                                                                                                                                                                                                                                                                                                                                                                        385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                   779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaggaagacttcgaggaagccaggaaggcactgaagctttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                                                                                                                                                                                                aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                    caagegeeteeaggtetetacaegaagaeeeaggaeeeageeaaageeeeeaaeaeeeet 660
                                                                                                                                                                                                                                                                                                  atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacccccaagaac
                                                                                                                                                                                                                                                                                                                                                           atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATC
GTATCTACGAGACCC
             gtatctacgagaccc 853
                                                        AGCATGGAGTGGGCCGTATTGACATCGTGGAGACCCGCTTCATTGGAATGACGTCCCGAG
                                                                      agcatggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgag
                                                                                                               ATGGCACCAACCA-CAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCA
                                                                                                                              atggcaccacccagacctccttggagctcttcatgtacctgaacgaagtcgcgggca
                                                                                                                                                                       GACATTCTCGAGATCGAGTTCAAAAACACGGGGTCCCTGTGAAGGTGACCAACGTCAAGG
                                                                                                                                                                                   gacattctcgagatcgagttcaaaa--aaggggtccctgtgaaggtgaccaacgtcaagg
                                                                                                                                                                                                                            CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAAAAAACCCT
                                                                                                                                                                                                                                                                                     ATGGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC
                                                                                                                                                                                                                                                                                                                                           ATGGAGTACGCAAAGCAACACGGGATTCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCACTGTATGAGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.0%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 817.8; DB 11; Length Pred. No. 4.9e-185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
--
                                                                                     838
                                                                                                                                                                                                                                                                                                                                                                         540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                 803
                                                                                                                                             778
                                                                                                                                                                        744
                                                                                                                                                                                                                                                                                       624
                                                                                                                                                                                                                                                                                                                   600
                                                                                                                                                                                                                                                                                                                                                                                                                                                         444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204
                                                                                                                                                                                                                                 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
```

```
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
BI258834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                рь
                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                 QУ
                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                Ωy
                                                     밁
                                                                                    Qy
                                                                                                                       Дb
                                                                                                                                                      ρy
                                                                                                                                                                                            밁
                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                    368
                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                      1 GCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                          8 gcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatcctcgtgt 67
acgatcaggtccggtttgagctcagctgctactcactggccccccagataaaggtcattg
                                                   tggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgccacaggaaagggga
                                                                                                                                             atgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgcaaacaag
                                                                                                                                                                                                                                                                                 acttcgaggaagccaggaaggcactgaagcttggggccaaaaaggtgttcattgagg 187
                                                                                                                                                                                                                                                                                                                                                    ACTTCGAGGAAGCCAGGAAGAAGCACTGAAGCTTGGGGCCCAAAAAGGTGTTCATTGAGG
                                                                                                                        ATGAGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 878)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
BI258834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI258834 878 bp mRNA EST 17-JUL-2001 602989646F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109251 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 827.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11264 row: k column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI258834.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.4 kb. Library prepared by Life Technologies."

a 250 c 246 g 157 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:5109251"
/clone_lib="NIH_MGC_12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:14815578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.4%;
98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4e-183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 809.8; DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ت.
د.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                           367
                                                                                                                                                               307
                                                                                                                                                                                                                                                                                                                                                                                                           60
                                                          360
                                                                                                                                                                                                                                                                      180
                                                                                                                              300
                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ģ
```

δÃ

В

Ş

Ş 밁 Š 밁

668 601 809 541 548 481

Вb Ş

660

727

787

밁 ρ 밁 δõ В

LOCUS BI256559

SOURCE KEYWORDS VERSION ACCESSION DEFINITION

ORGANISM

COMMENT

FEATURES

source

REFERENCE

AUTHORS JOURNAL

TITLE

δÃ

428

밁

망

421 488

DB 11;

Length 838;

2; Gaps

2

240

302

360

602

720

ű

```
361 ACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAGGTCATTG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctgatggagt 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acceaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaagcatggc 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAA-ACCCCTGACATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccctgacattc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaaccaagcgc 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGCAAAGCAACACGGGATTCCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCATGGATG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acgcaaagcaacacgggattcccatcccggtcacttcccaagaacccgttggagcatggatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAAGGTGACCAACGTCAAGGATGGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGGGCCGTATTGACATCGTGGAGAACCG-TTCCTGGGAATGAAGT-CCGAGGTATCTAC 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggtatctac 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGC 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcgagatcgagttcaaaaaaggggtccctgtg-aaggtgaccaacgtcaaggatggcacc 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gagaccccagcaggcaccatcctttaccatgctcatttaga 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI256559 838 bp mRNA EST 17-JUL-2001
602976921F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5116133 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 838)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI256559.1 GT:14811085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                Plate: LLAM11282 row: j column:
High quality sequence stop: 810.
                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, IcDNA Library Arrayed by: Incyte Genomics, Inc.
/note="Organ: cervix: Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life
                                                       /tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                                                    /clone="IMAGE:5116133"
/clone_lib="NIH_MGC_12"
                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                on/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 몽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΥ
                                                                                                                                                                                                                                                                                                                                                                   QΥ
                                                                                                                                                                                                                                                                                                                                                                                                           Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 827;
                                                                                                                                                                                                                                                                                               ρy
                                                                                                                                                                                                                                                                                                                                    망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                           DЬ
                                                                                                                                                                                        D
                                                                                                                                                                                                                      Qy
                                                                                                                  BI257913
                                                                            DEFINITION
                         VERSION
                                           ACCESSION
                                                                                                5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423 cattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctgat 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 GGAGTACGCAAAGCAACACGGGATTCCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 gtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatcct 62
                                                                                                                                                                                                                                                                                                                                  661 CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATGG
                                                                                                                                                                                                      783 tggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcc 834
                                                                                                                                                                                                                                                           721 CACCA-CCAACAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCA
                                                                                                                                                                                                                                                                               723 caccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaagca 782
                                                                                                                                                                                          780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           actgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTTGGGGCCAAAAAGGTGTTCAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTGGCCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccagaa 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggggaacgatcaggtocggtttgagctcagctgctactcactggccccccagataaaggt 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acaagtggaaatcgcccagcgggaggggggccaagtatgtgtcccacggcgcccacaggaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCAGATAAAGGT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagcat 542
                                                                                                                                                                                                                                                                                                                                                        cattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggatgg
                                                                                                                                                                                                                                                                                                                                                                                                           AGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAAGCCCCCAAAAAGCCCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                              agogoctocaggtototacacgaagacocaggacocagocaaagcococaacacocotga 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGCGTGGGCCGTATTGACATCGTGGAGAA-CGCTTCATTGGAATGAAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                           mRNA sequence.
BI257913
                                                                              B1257913 875 bp mrNA EST 1/-001-2001
602970844F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5110307
                         BI257913.1 GI:14813752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Technologies."
237 c 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 803.2; DB 1 pred. No. 1.5e-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 t
```

```
γQ
                                                                                                                                      밁
                                                                                                                                                                        Ş
                                                                                                                                                                                                             Ъ
                                                                                                                                                                                                                                               γ
                                                                                                                                                                                                                                                                                       Db
                                                                                                                                                                                                                                                                                                                        Оy
                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
481 atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc 540
                                       440 GTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTG 499
                                                         421 gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg 480
                                                                                                              380 AAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAG 439
                                                                                                                                  361 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
                                                                                                                                                                                      320 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGA 379
                                                                                                                                                                                                         301 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga 360
                                                                                                                                                                                                                                                                 260 GCACTGTATGAGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC
                                                                                                                                                                                                                                                                                   241 gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc 300
                                                                                                                                                                                                                                                                                                                                        140 AAGGAAGACTTCGAAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGGGGCCAAAAAGGTGTTC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                   121 aaggaagacttcgaggaagccaggaaggacgcactgaagcttgggggccaaaaaggtgttc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 CTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGGCCTATCTGGCCCAACATTGGCCAG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ctcgtgtggggtggaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://image.llnl.gov
Plate: LLAW11267 row: g column: 12
High quality sequence stop: 871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 875)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.4 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:5110307"
/clone_lib="NIH_MGC_12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ∕organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.2%;
97.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 783; DB 11; Length 875; Pred. No. 1e-176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Gaps
                                                                                                                                                                                                                                                                   319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.
```

```
ORIGIN
                   BASE COUNT
                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI260468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΨ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         858 AGTATCTAACGGAGACC 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          838 ggtatctacgagacccc 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 798 ACCATGGCGTGGGCCGTATTGACATCGTGGAGAAACCGGTTCATTGAATTGAAGTCCCGA 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     779 agcatggcgtgggccgtattgacatcgtggag-aaccgcttcattggaatgaagtcccga 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       721 9gcaccaccaccagacctcctt-ggagctcttcatgtacctgaacg-aagtcgcgggca 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            661 gacattetegagategagtteaaaaaaggggteeetgtgaaggtgaeeaaegteaaggat 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    620 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAAAGCCCCC--AAACCCCCT 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601 caagegeetecaggtetetacaeggaagaeecaggaeeceaggeeaaaggeeeceaaeaeeeeet 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 atggatgagaacctcatgcacatcagctacgaggctggaatcctggaggaaccccaagaac 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       560 ATGGÁTGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop:
                                                                                                                                                                                                                                                               http://image.llnl.gov
Plate: LLAM11263 row:
                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                602969267F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5108729 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI260468.1 GI:14818793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI260468
     note="organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.4 kb. Library prepared by Life
Technologies."
a 236 c 232 g 143 t
                                                                                          /tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                                                                                             /clone="IMAGE:5108729"
/clone_lib="NIH_MGC_12"
                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                              . 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  815 bp
                                                                                                                                                                                                                                                           row: e column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                           791.
```

Query Match

Local Similarity

63.0%;

Score 780.6; DB 11 Pred. No. 3.7e-176;

DB 11;

Length 815;

Ър γQ 밁 ρy 밁 Ş

```
RESULT
BE379161
                                                                                     SOURCE
ORGANISM
                             REFERENCE
                                                                                                                           KEYWORDS
                                                                                                                                               VERSION
                                                                                                                                                                ACCESSION
         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                    781
                                                                                                                                                                                                                                                                                                                                                       780
                                                                                                                                                                                                                                                                                                                                                                                             721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481
                                                                                                                                                                                                                                                                                                                                                                                                                               720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccctga
                                                                                                                                                                                                                                                                                                                                 gca-tggcgtgggccgtattgacatcgtggagaac 813
                                                                                                                                                                                                                                                                                                                                                                                                           tggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATTCTCGAGATCGAGTTCAAAACAACAGGGGGTCCCTGTGAAGGTGACCAACGTCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cattctcgagatcgagttcaa---aaaaggggtccctgtgaaggtgaccaacgtcaagga
                                                                                                                                                                                                                                                                                                                GCATTGGCGTGGGCCGTATTGACATCGTGGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                     TGGCACCGACCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGTACGCAAAGCAACACGGGATTCCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99agtacgcaaagcacacgggattcccatcccggtcactcccaagaacccgtggagcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctgat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9999aacgatcaggtccggtttgagctcagctgctactcactggccccccagataaaggt 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAAGTGGAAATCGCCCAGCGGGAGGGGCCCAAGTATGTGTCCCACGGCGCCCACAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgcccacaggaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGGGGCCAAAAAGGTGTTCAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttcat 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cgtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccagaa 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtccagcaaaggctccgtggttctggcctacagttggcggcctggacacctcgtgcatcct 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTGGCCAGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           807;
                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 980)
                                                                                                                                                              mRNA sequence.
BE379161
                                                                                                                                                                                              BE379161 980 bp mRNP
601238137F1 NIH_MGC_44 Homo
         NIH-MGC
                                                                                   Homo sapiens
                                                                                                                                           BE379161.1 GI:9324526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
       http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                sapiens cDNA clone
                                             Catarrhini;
                                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                           Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                IMAGE: 3610088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                ر.
د
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ŋ
                                         DЬ
                                                                           δÃ
                                                                                                                   В
                                                                                                                                                       Qy
                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                        QΥ
                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                      Ър
                                                                                                                                                                                                                                                                                                                                                 Вр
                                                                                                                                                                                                                                                                                                                                                                                                                           Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
     807
                                         481
                                                                                                                   421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                            361
                                                                                                                                                                                                                                627
                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                                   507
                                                                                                                                                                                                                                                                                                                                                                                                                                                               447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 gggcacctctcttgccaggccctgcatcgcccgcaaacaagtggaaatcgcccagcggga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 | GGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAACAACAAGTGGAAATCGCCCAGCGGGA
                                                                                                                                                                                        gacccaggacccagccaaagcccccaacacccctgacattctcgagatcgagttcaaaaa
                                                                                                             GCTCTTCATGTACCTAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGT
                                                                                                                                                                                                                                                                                      ctacgaggctggaatcctggagaaccccaagaaccaagcgcctccaggtctctacacgaa
                                                                                                                                                                                                                                                                                                                                                                 tcccatcccggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcag
                                                                                                                                                                                                                                                                                                                                                                                                                       ATTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                           attctacaaccggttcaagggccgcaatgacctgatggagtacgcaaagcaacacgggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCAGCTGCTACTCACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gctcagctgctactcactggccccccagataaaggtcattgctccctggaggatgcctga 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGA
ggagaaccgcttcattggaatgaagtcccgaggtatctacgaga-ccccagcaggcacca
                                                           gctcttcatgtacctgaacgaagtcgcgggcaagcatggcgtgggccgtattgacatcgt 806
                                                                                                                                                                                                                                                                      CTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCTACACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99999ccaagtatgtgtcccacggcgccacaggaaaggggaacgatcaggtccggtttga
                                                                                                                                                                                                                                                                                                                                             TCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM265 row: j_column: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.0%;
Similarity 93.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Institutes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).' a 297 c 261 g 182 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:3610088"
/clone_lib="NIH_MGC_44"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 780.2; DB 10; Pred. No. 4.8e-176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
```

밁 δÃ Ъ Q 망 Q В δÃ Вb δÃ Вp ρy B Qy

β 망 Qy Вb δÃ В Qy

밁

480

566

240

300

360

180

386

60

```
RESULT
BG828136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctgagtgtgaatttgtccgccactgcatc--gccaagtcccaggagcgagtgg-aaggga 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tectttaceatgeteatttagaeategaggeetteaceatggaeegggaagtgegeaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCACTGATTCCCCCCGGGTCATCAACACTCATTCCCCCCAGCTGAAGAGAAT 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caactgatgccaccgggttcatcaacatcaattccctcaggctgaaggaat 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tgtctctctacaatgaggag-----ctggtgagcatgaacgtgcagggtgat-tatgagc 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aagtgcaggtgtccgtcctcaagggcc---aggtgtacatcctcggccgggagtccccac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGAGTGTGAATTTGTCCGCCACTGCATCCGCCAAGGTCCCAGGAGCGAGTGGCACGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTCTGGCACAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tcaaacaaggcctgggcttgaaatttgctgagctggtgtataccggtttacggcctagcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGTCTCTCTTACATGAGGAAGCCTGGTGACCCTTGACGTGCACGGTGATCTATGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGTGCAGGTGTCCGTCCTCAAGGGGCCAGGTGGTTCATTCCTCGGCCGGGAAGTCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
Plate: LLCM1808 row: 1 column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BG828136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG828136.1 GI:14175723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602753522F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4906132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 905)
                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 790.
Location/Qualifiers
                         Ø
               /tissue_type="rhabdomyosarcoma"
/tissue_type="rhabdomyosarcoma"
/tab_host="DHIOB (phage resistant)"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
/note="Organ: muscle; Vector: pOTB7; Sites using the Directionally cloned into EcoRI/XhoI sites using the Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGACGAG(G), Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 265 c 253 g 160 t
                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4906132"
/clone_lib="NIH_MGC_17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   905 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ر.
د
```

```
Qy
                                                         DЬ
                                                                                   Qy
                                                                                                                    Db
                                                                                                                                              Qy
                                                                                                                                                                              Db
                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                           Дb
                                                                                                                                                                                                                                                                     ρy
                                                                                                                                                                                                                                                                                                     Ъ
                                                                                                                                                                                                                                                                                                                                  Ωy
                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 851
                                                                                                                                                                                                                                                                                                                                                                507
                                                                                                                                                                                                                                                                                                                                                                                              480
                                                                                                                                                                                                                                                                                                                                                                                                                             447
                                                                                                                                                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147
 861
                840 tatctacgagaccccagcaggcaccatcctttacca
                                                                                                                                                                                                                                             627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300
atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacgggcgccacagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaa-aaggtgtt 179
                                                                         gcatggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgagg
                                                                                                                      TGGCACACCACCAGA---CTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAA
                                                                                                                                                                                 TGACATTCTCGAGATCGAGTTCAAAACAAGGGGTCCTGTGAAGGTGACCAACGTCAAGGA
                                                                                                                                                                                                                                             CCAAGCGCCTCCAGGTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAA-ACCCC
                                                                                                                                                                                                                                                        ccaagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccc
                                                                                                                                                                                                                                                                                                        CATGGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAA
                                                                                                                                                                                                                                                                                                                     catggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaa
                                                                                                                                                                                                                                                                                                                                                                  GATGGAGTACGCAAAGCAACACGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                gatggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggag
                                                                                                                                                                                                                                                                                                                                                                                                                               GGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCCGCAATGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                             ggtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cgcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGGGCCCAAACAAGGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctcgtgttggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATC 86
                                                           GCATGGCGTGGGCCGTATTGACATCGTGGAGAACCG-TTCATGGGAATGAAGTCCC-AGG
                                                                                                                                                                                                 tgacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaagga
                                                                                                                                   tggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaa 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.3%;
97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 772.4; DB 11; Pred. No. 3.5e-174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419
                                                                                                                                                                                                              719
                                                                                                                                                                                                                                                                                                                                      599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446
                                                                                                                                                                                                                                                                                                                                                                                                  539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359
                                                                                         839
                                                                                                                                                                                                                                                                                                        626
                                                                                                                                                                                                                                                                                                                                                                                                                                                             479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
                                                                                                                        802
                                                                                                                                                                                   745
                                                                                                                                                                                                                                              685
                                                                                                                                                                                                                                                                           659
                                                                                                                                                                                                                                                                                                                                                                                                                                506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206
```

RESULT BI259920

LOCUS DEFINITION

ACCESSION

mRNA sequence. BI259920

BI259920 918 bp 602968961F1 NIH_MGC_12

mRNA Homo

sapiens cDNA clone

17-JUL-2001 IMAGE:5108463

<u>ن</u>

```
р
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
726 cacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaagcatgg 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                       666 tetegagategagtteaaaaaaggggteeetgtgaaggtgaecaaegteaaggatggeae 725
                                                                       361 retegagategagtteaaaaaaagggteeetetgaggtgaeeaaegtaaggategeae
                                                                                                                                   301 GCCTCCAGGTCTCTACACGAAGACCCAGGACCCAAGCCAAAAGCCCCCAACACCCCTGACAT 360
                                                                                                                                                                                                   241 TGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAACCAAGC 300
                                                                                                                                                                                                                     546 tgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaaccaagc 605
                                                                                                                                                                                                                                                                                     486 gtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagcatgga 545
                                                                                                                                                                                                                                                                   181 GTACGCAAAGCAACACGGGATTCCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCATGGA 240
                                                                                                                                                                                                                                                                                                                                    121 GCCTCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGA 180
                                                                                                                                                                                                                                                                                                                                                       427 g-ctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctgatgga 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                      367 aacgatcaggtccggtttgagctcagctgctactcactggccccccagataaaggtcatt 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 gaaatcgcccag-cgggagggggccaagtatgtgtcccacg-gcgccacag-gaaagggg 366
                                                                                                                                                                                                                                                                                                                                                                                                  61 AACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCAGATAAAGGTCATT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAAATCGCCCAGCCGGGAGGGGCCAAGTATGTGTCCCACGTGTGCCACAGAGAAAGGGG 60
                                                                                                                                                     9cctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccctgacat 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oca1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://image.llnl.gov
Plate: LLAM11262 row: j column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTH-MGC http://mgc.nci.nih.gov/.
mational Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI259920.1 GI:14817719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note="organ: cervix; Vector: pcMV-SpoRT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NIH_MGC_12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:5108463"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.1%; Score 768.8; DB 11; 95.6%; Pred. No. 2.5e-173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
```

В

В

DЬ δõ В Ş Дb Ş DЬ δõ

```
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE378581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ДЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1202 aatatcatcgtctcca 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1143 tgattatg-agccaactgatgccaccgggttcatcaacatcaattccctcaggctgaagg 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1083 cggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcaggg 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           901 ACTATCATCGACTCCA 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    841 TGATCATGAAGCCAATGAATĠCCAACCGAGTCATCAACATCAATTCCCTCACGCTGAAGG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        781 TCGGCCGGGAATCCCCATGTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCCGGA 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    965 ataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgcc-aagtcc 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661 ATACCGGTTTCTGGCACAGCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 GGACCGGGAAGTGCGCAAAATCAAACAAGGCCTTGGGCTTGACAATTTGCTGAGCTGGTGT 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          906 9gaccgggaagtgcgcaaaatcaaacaaggcctgggcttga-aatttgctgagctggtgt 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 CGAGACCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCAT 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 CGTGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             786 cgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggtatcta 845
                                                                                                                                                                                                                                                   cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: Plate: LLCM262 row: n column: 09
                                                                                                                                                                                                                                                 High quality sequence stop: 766
                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 952)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE378581 952 bp mrNA EST 21-JUL-2000 (01236939F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609032 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE378581.1 GI:9323946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="endometrium, adenocarcinoma cell line"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="BH10B (phage-resistant)"
/note="DH10B (phage-resistant)", Site_1: XhoI; Site_2:
/note="DH3 made by oligo-dT priming. Directionally
ECORI; CDNA made by oligo-dT priming. Directionally
adaptor: GGCACGAG(6). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:3609032"
/clone_lib="NIH_MGC_44"
                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primates; Catarrhini; Hominidae; Homo.
```

```
BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               융
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                   ρ
                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                    밁
                                                                                                                                                                                                Š
                                                                                                                         Q
                                                                                                                                            В
                                                                                                                                                             Qy
                                                                                                                                                                                 В
                                                                                                         В
                                                                                      QΥ
                                                                     망
                                                  QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GCTCAGCTGCTACTCGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGA 180
                                                                                                                                                                                                                                                                                                                                                                  447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POCGT
                                                                                                                                                                                                                                                                                                                                                                            507 tcccatcccggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcag 566
                                                                                                                                                                                                                                                                                                                                                                                                       181 ATTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGACTACGCAAAGCAACACGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                              421
                                           1047 gcaggtgtccgtcctcaagggccaggtgtacatcctcggccggggagtccccactgtctct 1106
                                                                                                                                                                                   541
                                                                                                                                                                                                                       481
                                                                                                                                                                                                                                        747
                1107 ctacaatgagga 1118
                                                                                                          660 CAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTCTGGCACAG-CC 718
                                                                      719 TGAGTGTGAATTTGTCCG-CACTGCATCGCCAAGTCCCAGGAGCGAAGTGGAAGGAAAGT 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              778 GCAGGTGTCCGCCTCCA---GGCAGGTGTACATCCTCGGCGGATTCCCATGTCTCTCTCA 834
835 TGAGAGTGGTGA 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                   gctcagctgctactcactggcccccagataaaggtcattgctccctggaggatgcctga 446
                                                                                                                                                                                                                                                                                                                                                                                                                attctacaaccggttcaagggccgcaatgacctgatggagtacgcaaagcaacacgggat 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         820;
                                                                                                                                                                                                                                                                  CCTTTACCATGCTCATTTAGACATCGAGG-CTTCACCATGGACCGGGAAGTGCGCAAAAT 659
                                                                                                                                                       cctttaccatgctcatttagacatcgaggccttcaccatggaccgggaagtgcgcaaaat 926
                                                                                                                                                                                                                      GCTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCCTGGGCCGTATTGACATCGT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 61.2%;
Similarity 96.2%;
                                                                               tgagtgtgaatttgtccgccactgcatcgccaagtcccaggagcgagtggaagggaaagt 1046
                                                                                                                     caaacaaggcctgggcttgaaatttgctgagctggtgtataccggtttacggcctagccc 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 275 c 266 g 176 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 758.4; DB 10 pred. No. 7.7e-171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Gaps
```

```
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                   Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                             143 AAGGAAGACTTCGAAGGAAGGCAGGAAGAAGGCACTGAAGCTTGGGGGCCAAAAAAGGTGTTC 202
                                                                                                                                                                                                                                                                                                                                                                                   Local
241 gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc 300
                                                                                                                                                                                                                                   203 ATTGAGGATGTCAGCAGGGAGTTTGTGGAGGAGTTCATCTGGCCCGGCCATCCAGTCCAGC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B1085601 881 bp mRNA B1085601 NIH_MGC_98 HOMO sapiens cDNA clone IMAGE:5013131 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI085601.1 GI:14503931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             825; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Sequencing by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics information can be Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plate: LLCM1818 row: f column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://image.llnl.gov
                                                                                                                      dCACTGTATGAGGACCGCTACCTCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xrel="caxo"."
/clone=lib="NHACE:503131"
/clone=lib="NHACE:503131"
/clone=lib="NHACE:503131"
/clone=lib="NHACE:503131"
/clone=lib="NHACE:503131"
/tissue_type="astrocytoma grade IV, cell line"
/tissue_type="astrocytoma grade IV, cell line"
/tissue_type="astrocytoma grade IV, cell line"
/tissue_type="astrocytoma grade IV, coll in cell line"
/tissue_type="astrocytoma grade IV, collowing 5"
/conte "organ: bradn; vector: priming the following 5'
/cloned into EcoRI/XhoI sites using the following 5'
/clone=lib="astrocytoma grade IV, cell line"
/tissue_type="astrocytoma grade IV, cell line"
/tissue_type=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.8%; Score 753.2; DB 11; Length 881; 96.2%; Pred. No. 1.3e-169; ______
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
```

```
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF206265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ъ
                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                863 GAGGTATCTAGAGAACCC 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               836 gaggtatctacgagaccc 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                803 GCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAAACGGTTCATTGGCACTGAAGTCC 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        717 ggatggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtc-gcgg 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 659 ctgacattctcgagatcgagttca-aaaaaggggtcoctgtgaaggtgaccaacgt-caa 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             683 CTGACATTCTCGAGATCGAGTCCACACAAAGGGGTCCCCTGTGAAGGTCACCAACGTCCAA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   599 accaagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacaccc 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  623 ACCAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCAGACAAAGACCCCCAAGACCC 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540 catggatgagaacctcatgcacatcagctacgaggctggaatcctggag-aaccccaaga 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        563 CATGGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAAACCCCGAAGA 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              503 GATGGAGTACGCAAAGCAACGGGATTCCCCATCCCGGTCACTCCCCAAGAACCCGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                480 gatggagtacgcaaagcaacacgggattcccatcccggtcactccccaagaacccgtggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420 99tcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacct 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443 GGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAAGCGGTTCAAGGGCCGCAATGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 ACAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 a-aggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaa 419
                                                                                                                                                                                             Plate: LLCM964 row: g column: 19 High quality sequence stop: 722.
                                                                                                                                                                                                                   cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9caagcatggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtccc 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGACTGGAGCAACCGACAGAACTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCAGGGG 802
                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF206265.1 GI:11099851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601869276F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4098090 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF206265
/Clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="0rgan: brain; Vector: pOTB7; Site_1: Xho1; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
                                                                                                           /clone="IMAGE:4098090"
                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1028 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
```

```
Qγ
                                                  밁
                                                                           QΥ
                                                                                                           Ъ
                                                                                                                                      Qy
                                                                                                                                                                        В
                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                Дb
                                                                                                                                                                                                                                                                                                                           Qγ
                                                                                                                                                                                                                                                                                                                                                           DЬ
                                                                                                                                                                                                                                                                                                                                                                                       δõ
                                                                                                                                                                                                                                                                                                                                                                                                                       Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
839 gtatctacgagaccccagcaggcaccat 866
                    813 AGCATGGAGTGGGCCGGAATGACATCGGGGAGAACCGCT--CATGGAATTGAAGCCCCCAG 870
                                      779 agcatggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgag 838
                                                                               753 TEGGACCAGCCAACAGAACCTCCTTGGAGCTCTCAAGGTACCTGAGCGAAAGTCCGGGCA 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                 720 tggcaccaccaccagag-acctccttggagctcttcatgtacctgaacgaagtcgcgggca 778
                                                                                                                                          693 GACATTOTOGAGATOGAGTTOAAAAAAAGGGGTCCCCGGGGAAACGTGAACAACGGTCAGGA 752
                                                                                                                                                           661 gacattctcgagattcgaagatggggtccctgtg-aaggtgaccaacgtcaagga 719
                                                                                                                                                                                                      634 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAAGCCCAAAGCCCCCAAGA-CCCT 692
                                                                                                                                                                                                                       601 caagcgcctccaggtctctacacggaagacccaggacccagccaaagcccccaacacccct 660
                                                                                                                                                                                                                                                                                 541 atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacccccaagaac 600
                                                                                                                                                                                                                                                                   574 ATGGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAAATCCTGGAGAAACCCCCAAGAAC 633
                                                                                                                                                                                                                                                                                                                                 514 ATGGAGTACGCAAAGCAACATGGGATTCCCCATCCCGGTCACTCCCCAAGAACCCGTGGAGC
                                                                                                                                                                                                                                                                                                                                             481 atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc 540
                                                                                                                                                                                                                                                                                                                                                                                           454 GTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTG 513
                                                                                                                                                                                                                                                                                                                                                                                                          421 gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 AÁGGGGAÁCGATCAGGTCCGGTTTGAGCTCAGCTGGTACTCACTGGCCCCCCAGATAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 AAGGAAGACTTCGAGGAAGCCAGGAAGAAGCACTGAAGCTTGGGGGCCAAAAAAGGTGTTC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 aaggaagacttogaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 CTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGGCCTATCTGGCCAACATTGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ctcgtgtgggtggaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGGGGGGCTGGACACCTCGTGCATC 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCACTGTATGAGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC_Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 749.2; DB 11;
Pred. No. 1.2e-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Gaps
                                                                                                                                                                                                                                                                                                                                 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                           453
```

871 GAACCACGAGGACCCCGGAGGACACCCT 898

Page

10

BI253774 DEFINITION

12

SOCOS

mRNA sequence. BI253774

BI253774.1 GI:14805532

SOURCE KEYWORDS ACCESSION

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Unpublished (1999) Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

NIH-MGC http://mgc.nci.nih.gov/

FEATURES

High quality sequence stop: 815. Location/Qualifiers

/db_xref="taxon:9606" /clone="IMAGE:5115413" /clone_lib="NIH_MGC_12" /organism="Homo sapiens" Plate: LLAM11280 http://image.llnl.gov

row: 1 column: 06

source

ORIGIN BASE COUNT

251 c

255 g

163 t

Query Match

Local

Similarity Conservative

0;

Mismatches

360;

р Š

οy

Дb 80 Вþ

₽ 20

DЬ

257

317

```
121 aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc 180
                                                                                                                                                                                  138 AAGGAAGACTTCGAGGAAGCCAGGAAGAAGCACTGAAGCTTGGGGCCCAAAAAGGTGTTC 197
                                                                                                                                                  241 gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc 300
                                                                                                                       18 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATC 77
                                                                                                                                                                                                                                                                                                                            1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602976122F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5115413 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 898)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institutes of Health, Mammalian Gene Collection (MGC)
               GCACTGTATGAGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 316
AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                              60.4%; Score 748.6; DB 11, 96.7%; Pred. No. 1.7e-168;
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length 898;
                                                                                                                                                                                                                                                                                                                                                                                         19; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            뭉
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
BI258628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 GGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             660 tgacattotogagatogagttoaaaaaaggggtocootgtgaaggtgaocaacgtcaagga 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  557 CATGGATGAGAACCTCATGGACATCAGCTACGAGGCTGGAATCCTGGAGAA-CCCAAGAA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             851 GTATCTACGAGA-CCCAGGAGGCACATTCTTTACCATGCTCATTTAGA 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     839 gtatctacgagaccccagcaggcaccatcctttaccatgctcatttaga 887
                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacct 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaa 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtc-gcgggca 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI258628 851 bp mRNA EST 1/-JUL-2011
602969566F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109064 5',
                                                                                                                                                                                                                                                                                                                                                                 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 851)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI258628.1 GI:14815170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
                                                                                                                                                         High quality sequence stop: 849.
                                                                                                                                                                             http://image.llnl.gov
plate: LLAM11264 row: c column: 17
                                   /tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                                /clone="IMAGE:5109064"
/clone_lib="NIH_MGC_12"
                                                                                                   /db_xref="taxon:
                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                     /note="Organ: cervix; Vector: pcmV-SPORT6; Site_1: NotI;
                                                                                                                                               Location/Qualifiers
```

```
836 TCTATTGAGACCC 848
                                    841 atctacgagaccc 853
                                                        781 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                          778 CATGGCGTGGG-CGTATTGACATCGTGGAGAACCG-TTCATTGGAATGAAGTCCGAGGTA 835
                                                                                        660 CATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCTGTGAAGGTTGACCAACGTCAAGGATG 719
                                                                                                                                                      663 cattotogagatogagttomamamaggggtocotgtgmagg-tgmoccaacgtomaggatg 721
                                                                                                                                                                                         601 AGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGGCCAAAGCCCCCAA-AACCCTGA 659
                                                                                                                                                                                                      603 agcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccctga 662
                                                                                                                                                                                                                                        541 GGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCA 600
                                                                                                                                                                                                                                                     543 ggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaacca 602
                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                       421 CATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTGAT 480
                                                                                                                                                                                                                                                                                                                                                     423 cattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctgat 482
                                                                                                                                                                                                                                                                                                                                                                                       361 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAGGT 420
                                                                                                                                                                                                                                                                                                                                                                                                     363 9999aacgatcaggtccggtttgagctcagctgctactcactggccccccagataaaggt 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 acaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacaggaaa 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 actgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgcaa 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 ACTGTATGAGGACCGCTACCTCCTGGGCACCTCTTGGCAGGCCCTGCATCGCCGGCAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGGGCCCAAAAAAGGTGTTCAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 9gaagacttcgaggaagccaggaaggcactgaagcttggggccaaaaaggtgttcat 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 cgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccagaa 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Grecageanaggerecerrecerregeeracagregeegeeregaeaceregeareer 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 gtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatcct 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTGGCCAGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 60.2%;
Similarity 96.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 745.4; DB 11; Length 851; Pred. NO. 9.5e-168; 0; Mismatches 21; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
Ъ
                     δÃ
                                               Ъ
                                                                     Qy
                                                                                               Ъ
                                                                                                                     δÃ
                                                                                                                                               Дb
                                                                                                                                                                     Qγ
                                                                                                                                                                                               В
                                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                             ДЪ
                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI258439
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                     Local
```

밁

Дb Š 밁 Ş В δÃ 밁 Š DЬ Ş Дb Ş Дδ δÃ DЬ Ş В δ В Ş DЬ δõ DЬ δõ В Ş B

```
Query Match
386 AAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAG 445
             361 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
                                                          326 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGGCCAAGTATGTGTCCCACGGGGGCGCCACAGGA 385
                                                                           301 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga 360
                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                146 AAGGAAGACTTCGAGGAAGGCAGGAAGAAGGCACTGAAGCTTGGGGCCCAAAAAAGGTGTTC 205
                                                                                                                                                                                                                                                              121 aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                         86 CTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGGCTATCTGGCCAACATTGGCCAG 145
                                                                                                                                                                                                                                                                                                                          61 ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                     829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: LLAM11271 row: i column: 06 High quality sequence stop: 781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11271 row: i column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI258439.1 GI:14814785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602972421F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5111885 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI258439
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note-"organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.4 kb. Library prepared by Life Technologies."

263 c 249 g 160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:5111885"
/clone_lib="NIH_MGC_12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.8%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              894 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 741; DB 11; Length 894; Pred. No. 1.1e-166;
                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  9
```

B δõ

Š В

망 20 В

δÃ 망 Q

215 a

241 c

240 g

155 t

```
멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI255104
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 566 ATGGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAAATCCTGGAGAACCCCCAAGAAC 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            778 aagcatggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccga 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             744 TGGCACCAACAGAACCTTCCTGGAGCTCTTCATGTACCTTGAACGGAAGTTGCGGGC 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          804 CAGCCATGCGTTGGGCCGTTTGACATCGTGGAGAACCG-TTCTTTGGAATGAAGTCCCAA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       863 GGTAT-TACGAGACCCAAAGGCCCACCTTAC 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              838 ggratctacgagaccccagcaggcaccatcc 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac 600
                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tggcaccaccaccagacctccttggagctcttcatgtacct--gaacgaagtcgcgggc 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI255104 851 bp mRNA EST 17-JUL-2001 602975950F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5115204 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
BI255104
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 851)
                                                                                                                                                                                                                                                                                                                                                                                                                         BI255104.1 GI:14808181
                                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC
                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                        High quality sequence stop: 770.
                                                                                                                                                                      Plate: LLAM11280 row: c column: 13
/note-"Organ: cervix; Vector: pCMV-SpORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally, primer: Oligo dT site_2: salI; cloned unidirectionally, primer tife average insert size 1.4 kb. Library prepared by Life Technologies."
                                                     /clone="IMAGE:5115204"
/clone_lib="MIH_MGC_12"
/clone_tib="MIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ఠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Šõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   рb
                                                                                                                                                                                                                                                                                                                                                                                                    Q
                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                             Вþ
                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                        Вp
                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                         멍
                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                            δÃ
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                      밁
search completed: February 12, 2002, 13:10:00
Job time: 1713 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 acttcgaggaagccaggaagaaggcactgaagcttgagggccaaaaaggtgttcattgagg 187
| 128 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 129 | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          488 acgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagcatggatg 547 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 AGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAA-CCCAAGAACCAAGCGC 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        668 togagatogagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggatggcacca 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              659 TCGAGATCGAGTTCAAAAAAGGGGT-CCTGTGAGCGTGACCAACGTCAAGGATGTGACCA 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               718 CCCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGGAAGCATTGGC 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              728 cccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaagca-tggc 786
                                                                                                                                                                                                                                                                                                                                                                                      778 GTGGGCCGTATTGACCATCGGTTGGCACGAACCTGTTCACTTGGAATTGAAGTCCCCAAG 837
                                                                                                                                                                                                                       838 TATATACGAAAACC 851
                                                                                                                                                                                                                                                                                             840 tatctacgagaccc 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaaccaagcgc 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtgggccgtattgacatcgtggagaaccg-----cttcattggaatgaagtcccgagg 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 738.8; DB 11;
pred. No. 3.6e-166;
0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ري
د.
```

:				
			•	
			,	
				•
ļ!				
	- ·			

```
OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pending_Patents_NA_Main:*

1: /gqn2_6/ptodata/2/pna/PCTUS_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*

4: /gqn2_6/ptodata/2/pna/US080_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/US083_COMB.seq:*
February 12, 2002, 12:46:27; Search time 2570.39 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-775-693-1
1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17159718 seqs, 8763200856 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

(cgn2_6/ptodata/2/pna/US084_COMB.seq:*
(cgn2_6/ptodata/2/pna/US086_COMB.seq:*
(cgn2_6/ptodata/2/pna/US086_COMB.seq:*
(cgn2_6/ptodata/2/pna/US086_COMB.seq:*
(cgn2_6/ptodata/2/pna/US086_COMB.seq:*
(cgn2_6/ptodata/2/pna/US089_COMB.seq:*
(cgn2_6/ptodata/2/pna/US089_COMB.seq:*
(cgn2_6/ptodata/2/pna/US099_COMB.seq:*
(cgn2_6/ptodata/2/pna/US092_COMB.seq:*
(cgn2_6/ptodata/2/pna/US093_COMB.seq:*
(cgn2_6/ptodata/2/pna/US093_COMB.seq:*
(cgn2_6/ptodata/2/pna/US093_COMB.seq:*
(cgn2_6/ptodata/2/pna/US095A_COMB.seq:*
(cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
(cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
(cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
(cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
(cgn2_6/ptodata/2/pna/US096B_COMB.seq:*
(cgn2_6/ptodata/2/pna/US096B_COMB.seq:*
(cgn2_6/ptodata/2/pna/US096B_COMB.seq:*
(cgn2_6/ptodata/2/pna/US097B_COMB.seq:*
(cgn2_6/ptod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atgtccagcaaaggctccgt.....gcaaggtcactgccaaatag 1239
                                                        / cgn2_6/ptodata/2/pna/US600_COMB.seq: *
/ cgn2_6/ptodata/2/pna/US600_COMB.seq: *
/ cgn2_6/ptodata/2/pna/US6002_COMB.seq: *
/ cgn2_6/ptodata/2/pna/US6003_COMB.seq: *
/ cgn2_6/ptodata/2/pna/US6003_COMB.seq: *
/ cgn2_6/ptodata/2/pna/US6005_COMB.seq: *
/ cgn2_6/ptodata/2/pna/US6005_COMB.seq: *
/ cgn2_6/ptodata/2/pna/US6005_COMB.seq: *
/ cgn2_6/ptodata/2/pna/US6005_COMB.seq: *
/ cgn2_6/ptodata/2/pna/US6006_COMB.seq: *
/ cgn2_6/ptodata/2/pna/US6006_COMB.seq: *
/cgn2_6/ptodata/2/pna/US6010_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (without alignments)
8448.217 Million cell updates/sec
```

6/ptodata/2/pna/US6011_COMB.s
/ptodata/2/pna/US6012_COMB.s
_6/ptodata/2/pna/US6013_COMB.s
_6/ptodata/2/pna/US6014_COMB.s
_6/ptodata/2/pna/US6015_COMB.s
_6/ptodata/2/pna/US6016_COMB.
_6/ptodata/2/pna/
_6/ptodata/2/pna/
_6/ptodata/2/pna/US6019_COMB.s
_6/ptodata/2/pna,
_6/ptodata/2/pna/US6021_COMB.s
_6/ptodata/2/pna/US6022_COMB.s
_6/ptodata/2/pna/US6023_COMB.
_6/ptodata/2/pna/US6024_COMB.s
_6/ptodata/2/pna/US6025_COMB.s
_6/ptodata/2/pna/US6026_COMB.S
_6/ptodata/2/pna/US6027_COMB.s
_6/ptodata/2/pna/US6028_COMB.s
_6/ptodata/2/pna/US6029_COMB.s
n2_6/ptodata/2/pna/US6030_COMB.s
_6/ptodata/2/pna/US6031
/cgn2_6/ptodata/2/pna/US6032_COMB.seq:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

00	ο	0	٥		6) 6) 6)	6) 6) 6)	2111				Result No.
40	38	4 0 6	332	29 29 30	6 5 4	22 22	0 0 0	114	110	1004001	
731.6	892 828	1030 1012.4 913.2	1058 1058 1031.8	1199.6 1093 1093 1061	1199.6 1199.6 1199.6	1220 1200 1200	· w · ·	2222	1232.6 1232.6 1232.6 1232.6	1239 1232.6 1232.6 1232.6 1232.6 1232.6 1232.6	Score
59.0	200	83.1 81.7 73.7	ωσσ.	96. 88.2 85.6	96.8 96.8	98.5 96.9 96.9	99.5	99.55	99.55.55.55.55.55.55.55.55.55.55.55.55.5	100.0 99.5 99.5 99.5 99.5	Query Match
3017	2252 152425 1871	5018 104925 1541	191307 192305 3589	1989 164833 165831 4886	1828 1828 1828	1518 1808 1808	2812 1571 1836	1755 2057 2810 2812	1656 1656 1656 1725	1239 1656 1656 1656 1656	÷
25	- 5 5 4 4	57 60	555	55440	16 31	17	560	1 30	29 29 29	30 22 25 25 27 27	
92 142	-60-213-36 -60-212-66 -0801-0863	US-60-243-468-528 US-60-212-664-284 US-60-278-258-387	-60-216-7 -60-212-6 -60-207-2	US-60-216-770-49 US-60-212-664-46 US-60-243-468-420	-09-205-070 -09-340-623 -09-898-888	-60-164-285 -09-359-922- -09-359-922-	US-09-925-300-654 US-60-239-841-86 US-60-278-258-389	US-09-770-173-2339 US-09-760-475-983 PCT-US00-26524B-1903 PCT-US00-05988-654	-09	US-09-775-693-1 US-09-77410-7427 US-09-338-425-2021 US-09-652-126-9702 US-09-652-126-9327 US-09-698-010-14283 US-09-698-012-8607 US-09-698-012-8607	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
e 92, <i>1</i> e 142,	Sequence 630, App Sequence 165, App Sequence 4443, Ap		168, 342,	49, AI 46, AI	13594,		e 654, 7 e 86, Al e 389, 7	2339, 983, 1 1903, 1 654, AF	1274, 2581, 2755, 2021, 4186,	w	n

```
οy
                                                            Qγ
                  В
                                                                                                                 Db
                                                                                                                                                              Š
                                                                                                                                                                                                                  DЪ
                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                             δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens US-09-775-693-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-09-775-693-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09775693
GENERAL IMFORMATION:
APPLICANT: Clark, Mike
APPLICANT: Holtsberg, Frederick Wayne
APPLICANT: Holtsberg, Frederick Wayne
APPLICANT: Holtsberg, Frederick Wayne
APPLICANT: Ensor, Charles Mark
TITLE OF INVENTION: Methods For Predicting Susceptibility Of Patients To Arginine
TITLE OF INVENTION: Therapy
FILE REFERENCE: PHOE-0060
CURRENT APPLICATION NUMBER: US/09/775,693
CURRENT APPLICATION NUMBER: US/09/775,693
CURRENT APPLICATION SUBJECT OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
LENGTH: 1239
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 1239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 1239; DB 30; Length 1239; Best Local Similarity 100.0%; Pred. No. 1.5e-295;
                       541 atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac 600
                                                                                                                         481 atggagtacgcaaagcaacacgggattccccatcccggtcactccccaagaacccggtggagc
                                                                                                                                                                                                                                                                                                 361 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                 atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                          gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                      aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gcactgtatgaggaccgctacctcctgggcacctctcttgccaggcccttgcatcgccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaggaagacttcgaggaagccaggaaggaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aaggaagacttcgaggaagccaggaaggacgctcgaagcttggggccaaaaaggtgttc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    730
730
723.8
718.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctcgtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3017
3017
953
42519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
51
57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-60-185-362-59
US-60-185-362-126
US-60-243-468-1942
US-60-216-770-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                     480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59, Appl
126, App
1942, Ap
149, App
                                                                                                                                                                                                                                                                                                                                                                                                        360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dej
               ; ORGANISM: Homo sapiens US-09-577-410-7427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-577-410-7427; Sequence 7427, Application US/09577410; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
                                                                                                                   SOFTWARE: Fa
SEQ ID NO 7427
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gutter...
APPLICANT: Hodge, Martin
APPLICANT: Kingsbury, Gillian
APPLICANT: MacKay, Charles
APPLICANT: MacKay, Charles
APPLICANT: MacKay, Charles
                                                                                                                                                           APPLICANT: MacKay, Charles
TITLE OF INVENTION: Nucleic Acid Molecules Derived from
TITLE OF INVENTION: Nucleic Acid Molecules Derived from
TITLE OF INVENTION: Number cell, Bone Marrow, and CD34+ Libraries
FILE REFERENCE: 5800-32
CURRENT APPLICATION NUMBER: US/09/577,410
CURRENT FILING DATE: 1000-05-23
PRIOR FILING DATE: 1999-05-24
PRIOR APPLICATION NUMBER: US 60/135,632
PRIOR APPLICATION NUMBER: US 60/135,633
PRIOR APPLICATION NUMBER: US 60/135,633
PRIOR APPLICATION NUMBER: US 60/135,616
PRIOR APPLICATION NUMBER: US 60/135,616
PRIOR FILING DATE: 1999-05-24
PRIOR FILING DATE: 1999-05-24
PRIOR FILING DATE: 1999-05-24
PRIOR FILING DATE: 1999-05-24
NUMBER: OF SEQ ID NOS: 8991
COUNTRIES FOR TO SERVICE SERV
                                                                 TYPE: DNA
                                                                                            LENGTH: . 1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1201 gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1201 gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1141 ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1141 ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1081 ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1021 teccaggagegagtggaagggaaagtgeaggtgteegteeteaagggeeaggtgtaeate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        841 atctacgaggacccaggaggcaccatcctttaccatgctcatttagacatcgaggccttc 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                781 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721 ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9t9tataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99caccaccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gacattotogagatogagttoaaaaaaggggtocotgtgaaggtgaccaacgtcaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccct
                                                                                                                                           FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gutierrez-Ramos, Jose-Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  840
```

```
δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                        ρ
                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                   밁
                                                                                                                                                                                              δÃ
                                            В
                                                                       δÃ
                                                                                                        В
                                                                                                                                  δÃ
              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                                                                                                                    781 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 840
                                                991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaaggtgttc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgccacagga 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 510
                                                                                                                                                                                                                                                                                                                                                                                                                                    atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg 480
                                                                                                                                                                                                                                                                                                                                                                       caagggcctccaggtctctacacggagacccaggacccaggccaaagcccccaacacccct 660
                                                                                                                                                                                                                                                                                                                                                                                                                    atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc 540
                                                                                                                                                                                                                                                                                           gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat 810
                                                                                                                                                                                                                                                                                                           gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat 720
                                                                                                                                                                                                                                                                                                                                                          caagegeeteeaggtetetacaegaagaeeeaggaeeeageeaaageeeeeaaeeeeet
                                                                                                                                                                                                                                 ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag 870
                                                                                                                                                                                                                                              ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                           accatggaccgggaagtgcgcaaaatcaaaccaaggcctgggcttgaaatttgctgagctg
                                                                                                        atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                        atotacyagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc 900
                                                                                                                                                                  catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 930
gtgtatacoggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag 1020
                                           accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1232.6; DB 
Pred. No. 6e-294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 1622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                           960
                                                           1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
```

Дb

gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag

QΥ

```
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-338-425-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-338-425-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                     Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          γ
                                                                                                                                                                                                                                                                                                                                                                  Qγ
                                                                                                                                                                                                                          29
                                                                                                                                                                                                                                                               Вþ
                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2021, Application US/09338425 GENERAL INFORMATION:
                                                                                                                                                                                            멍
                                                                                                                         망
                                                                                                                                                        2
                                                      밁
                                                                                   ΩÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Shylan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILLE REPERENCE: 1600.2021-001
CURRENT APPLICATION NUMBER: US/09/338,425
CURRENT FILING DATE: 199-06-22
PRIOR APPLICATION NUMBER: 60/168,038
PRIOR FILING DATE: 1999-11-30
NUMBER OF SED ID NOS: 2814
NUMBER OF SED ID NOS: 2814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Williamson, Mark
APPLICANT: Shyjan, Andrew W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1081 ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1111 toccaggagegagtggaagggaaagtgcaggtgtccgtcctcaagggccaggtgtacatc 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1171 ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1291 gaatatcatcgtctccagagcaaggtcactgccaaatag 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1201 gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 184
                                                                                                                                                                                                                                                                                                                                                   121 aaggaagacttcgaaggaagccaggaagaaggcactgaagcttgggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                     185 ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                             y Match
Local Similarity 99.7%;
                                                                                                                                          301 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                          365 gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                         241 gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
421 gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                      361 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                        61 ctcgtgtgggtgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag 1200
                                                                                                                                                                                                                                                                                                                                .aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc 304
                                                    aaggggaacgatcaggtccggtttgagctcagctgctactcactggcccccagataaag
                                                                                                                       aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgcccacagga 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1232.6; DB 17; Length 1656; pred. No. 6.1e-294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                           360
                                     480
                                                                                                                                                                                                             424
```

US-09-652-126-9702

```
FILE REFERENCE: 1600.1185-001
CURRENT APPLICATION NUMBER: US/09/652,126
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,132
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 10051
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9702
SEQ ID NO 9702
TYPE: DNA
                                                                                                                                                                                                                                                                           US-09-652-126-9702
                                                                                                                                                                                                                                                                                                                                                                                                                   DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΩV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
                                                                                                                                                                                                                                          Sequence 9702, Application US/09652126 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                APPLICANT: Shyjan, Andrew W. TITLE OF INVENTION: NOVEL NUCTITIE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                    1201 gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    961 gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       905 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              665 atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac 600
                                                                                                                                                                                                                                                                                                                                   gaatatcatcgtctccagagcaaggtcactgccaaatag 1363
                                                                                                                                                                                                                                                                                                                                                                                                                  99tgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                               99tgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag 1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttggaaatttgctgagctg 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cat99c9t9g9ccgtattgacatcgt9gagaaccgcttcattggaatgaagtcccgaggt 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99caccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gacattotogagatogagttoaaaaaaggggtocotgtgaaggtgacoaacgtoaaggat 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 caagcgcctccaggtctctacacgaagacccaggacccagcccaagcccaagcccccaccccct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alggagtacgcaaagcaacacgggattcccattcccggtcactcccaagaacccgtggagc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg 604
                                                             FastSEQ for Windows Version 4.0
                                                                                                                                                                                                NOVEL NUCLEIC ACID MOLECULES AND
```

```
Дb
                                                                                            Qy
                                                                                                                            Db
                                                                                                                                                        Qy
                                                                                                                                                                                           멍
                                                                                                                                                                                                                       Ωy
                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                 ΩV
                                                                                                                                                                                                                                                                                                                  Вb
                                                                                                                                                                                                                                                                                                                                               ρy
                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δδ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ъ
                                              1025 accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 1235;
961 gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                               901 accatggaccgggaagtgcgcaaaatcaaagcaaggcctggggcttgaaatttgctgagctg
                                                                                                                         841 atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc 900
                                                                                                                                                                     905 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                        781 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                    845 ggcaccaccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                                                                                                               661 gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat 720
                                                                                                                                                                                                                                                                                                                                                                                                            601
                                                                                                                                                                                                                                                                                                                                                                                                                        665 atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 aaggaagacttcgaggaagccaggaaggactgaagcttgaagcttggggccaaaaaggtgttc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                           atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                     99caccacccacacagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                                                                                                                                                                                                                                                                gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l atgtocagcaaaggctccgtggttctggcctacagtggcgcctggacacctcgtgcatc 60
                                                                                                                                                                                                                                                                                                                                                            caagcgcotccaggtctctacacgaagacccaggacccagccaaagcccccaacacccct 784
                                                                                                                                                                                                                                                                                                                                                                             | caagegeetecaggtetetacaegaagaeeeaggaeeeaaggeeaaageeeeeaeaeeeee 660
                                                                                                                                                                                                                                                                                                                                                                                                                                          atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aagggaacgatcaggtccggttlgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.5%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1232.6; DB :
Pred. No. 6.1e-294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 25; Length 1656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                   1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304
```

```
APPLICANT: Gutierrez-Ramos, Jose-Carlos
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.11/7-001
CURRENT APPLICATION NUMBER: US/09/652,816
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,111
PRIOR APPLICATION NUMBER: 60/152,111
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9647
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9327
LENGTH: 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo
US-09-652-816-9327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-652-816-9327
                                                                                                                                                                                                                                                          γQ
                                                                                                                                                                                                                                                                                            Db
                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                        Вþ
                                                                                              망
                                                                                                                           δÃ
                                                                                                                                                               В
                                                                                                                                                                                        οy
                                                                                                                                                                                                                              멍
Qy
                                 밁
                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9327, Application US/09652816 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 1235; Conserv
     421
                                   485
                                                                                                  425
                                                                                                                                                                 365
                                                                                                                                                                                               241
                                                                                                                                                                                                                               305
                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                            245
                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                             185
                                                                                                                                                                                                                                                                                                                                                                                                                            125
                                                                                                                                301
                                                                  361
                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctcggccgggagtccccactgtctctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gaatatcatcgtctccagagcaaggtcactgccaaatag 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag 1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                         atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                                                                                                                                                            aaggaagacttcgaggaagccaggaágaaggcactgaagcttggggccaaaaaggtgttc 180
                                                                                                                                                                                                                                                                                                                                                                         ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                                                                        atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 184
                                                                                                                 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgcccacaga
                                                                                                                                                                                  gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                           aaggaagacttcgaggaagccaggaaggaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                           ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
 gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                  aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                               gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                   aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1232.6; DB 25;
Pred. No. 6.1e-294;
0; Mismatches 4; II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1200
                                                                                                                                                                    424
                                                                                                                                                                                                                                                                                                                                                              244
        480
                                                                                                                                     360
                                                                                                                                                                                                                                 364
                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                304
                                        544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
```

```
QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вþ
                                                                                                                                                                                                                                                                                                                                                                                             Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                       DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DЬ
                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                       ρy
                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                    Ωb
                        Ş
                                                    DЬ
                                                                           Qγ
                                                                                                       р
                                                                                                                              QΥ
                                                                                                                                                          Вb
                                                                                                                                                                                 QУ
                                                                                                                                                                                                           Вb
                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                             1085
                                                                                                       1205
                                                                                                                                 1081
                                                                                                                                                                                                                                                                1025
 1325
                                                                                                                                                                                    1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          545
                                                                                                                                                                                                                                                                                                                                                                                                                          845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      661
                                                                                                                                                                                                                                                                                        901
                                                                                                                                                                                                                                                                                                                                                                      905
                                                                                                                                                                                                                                                                                                                                                                                              781
                                                                                                                                                                                                                                                                                                                                                                                                                                                 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    accatggaccgggaagtgcgcaaaatcaaaccaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                     ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              caagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
            gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                     ctcggccgggagtccccactgtctctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                      gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                    catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                       ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
gaatatcatcgtctccagagcaaggtcactgccaaatag
                                                                                                       ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                        gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                             accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                     1140
                                                                                                                                                                                        1080
                                                                                                                                                                                                                                           1020
                                                                                                                                                                                                                                                                    1084
                                                                                                                                                                                                                                                                                                                     1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                604
                                                         1324
                                                                                                                                                               1204
                                                                                                                                                                                                                                                                                              960
                                                                                                                                                                                                                                                                                                                                                                           964
                                                                                                                                                                                                                                                                                                                                                                                                                              904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       724
                                                                                                                                                                                                                                                                                                                                                 900
```

```
RESULT 6
US-09-698-010-14283
J Sequence 14283, Application US/09698010
J Sequence 14283, Application US/09698010
J Sequence 14283, Application US/09698010
J Sequence 14283, Application Wark
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
J APPLICANT: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
J FILE REFERENCE: 1600.2029-001
CURRENT APPLICATION NUMBER: US/09/698,010
CURRENT FILING DATE: 2000-10-27
J CURRENT FILING DATE: 2000-10-27
J PRIOR APPLICATION NUMBER: 60/162,358
J PRIOR FILING DATE: 1999-10-29
J NUMBER OF SEQ ID NOS: 15684
J SOFTWARE: FastSEQ for Windows Version 4.0
J SEQ ID NO 14283
J LENCTH: 1656
```

; TYPE: DNA ; ORGANISM: Homo : US-09-698-010-14283

sapiens

```
밁
                              δÃ
                                                               밁
                                                                                     δÃ
                                                                                                                    В
                                                                                                                                         Qγ
                                                                                                                                                                         g
                                                                                                                                                                                                Qy
                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                     Ъ
                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                            Дb
                                                                                                                                                                                                                                                                                                                                                                    Ωy
                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        γO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
          1025
                                                                                                                    905
                                                                                                                                              781
                                                                                                                                                                                                     721
                                                                                                                                                                                                                               785
                                                                                                                                                                                                                                                          661
                                                                                                                                                                                                                                                                                                                601
                                                                                                                                                                                                                                                                                                                                                                                                 605
                                                                                                                                                                                                                                                                                                                                                                                                                            481
                                                                                                                                                                                                                                                                                                                                                                                                                                                       545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
             accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                    catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                         catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                               ggcaccaccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                               99caccaccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                      {\tt gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat}
                                                                                                                                                                                                                                     gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                                                                                                                                                                          caagegeetecaggtetetacaegaagaeeeaggaeeeageeaaageeeeeaeaeaeeeet
                                                                                                                                                                                                                                                                             caagegeetecaggtetetacaegaagaeeecaggaeeeageeaaageeeceaacaeeeet
                                                                                                                                                                                                                                                                                                                                  atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacccccaagaac
                                                                                                                                                                                                                                                                                                                                                  atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac 600
                                                                                                                                                                                                                                                                                                                                                                                       atggagtacgcaaagcaacacgggattccccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                      atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                             gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                          gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aaacaagtggaaatcgcccagcggggggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgcccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aaggaagacttcgaggaagccaggaaggacgcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aaggaagacttcgaggaagccaggaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctcgtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.5%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1232.6; |
Pred. No. 6.1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 27; Length 1656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
 1084
                                                                                                              964
                                                                                                                                                                                                                                                                                                         660
                                                       1024
                                                                                                                                                                  904
                                                                                                                                                                                                                         844
                                                                                                                                                                                                                                                                             784
                                                                                                                                                                                                                                                                                                                                                                                                                                                604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
```

```
Дb
                                                                                   Qy
                                                                                                                      В
                                                                                                                                                  ρy
                                                                                                                                                                                   Дb
                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                  망
                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                        QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA; ORGANISM: HOMO US-09-698-012-8607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-698-012-8607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ър
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QY
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 8607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8607, Application US/09698012 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/698,012
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/162,166
PRIOR FILING DATE: 1999-10-28
NUMBER OF SED ID NOS: 9719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HOITZMAN, DOUGLAS A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2002-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1656
                          361
                                                          425
                                                                                                                      365
                                                                                                                                                                                   305
                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                  125 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1081
                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                    185 ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                     61 ctcgtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
aaggggaacgalcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgcccacgga
                                                                                                                              gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgccgc
                                                                                                                                                                                          aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                       aaggaagacttcgaggaagccaggaaggcactgaagcttggggccaaaaaggtgttc
                                                aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgccacagga
                                                                                                            gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                            gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99tgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gaatatcatcgtctccagagcaaggtcactgccaaatag 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctcggccgggagtccccactgtctctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9t9tataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1232.6; DB 27; Length Pred. No. 6.1e-294;
                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1656;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                 484
                                                                                                                                                                                                                                        304
                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                     184
                                                                                                                                                                                                                                                                                                       244
                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
```

NOS:

```
APPLICANT: Hunter, John J.

APPLICANT: Shyjan, Andrew W.

APPLICANT: Stbdal, Hilde

TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USE

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 1600.2036-001

CURRENT APPLICATION UNMBER: US/09/710,281

CURRENT FILING DATE: 2000-11-10

PRIOR APPLICATION NUMBER: 60/164,254

PRIOR FILING DATE: 1999-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٠٥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db
                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   망
                                                                                                                                                                                                                                                                                                               Вb
                                                                                                                                                                                                                                                                                                                                           οy
                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                             RESULT 8
US-09-710-281-5043
Sequence 5043, Application US/09710281
GENERAL INFORMATION:
                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1025
                                                                                                                                                                                                                                                                                                                   1265
                                                                                                                                                                                                                                                                                                                                                                                                                                         1145
                                                                                                                                                                                                                                                       1325
                                                                                                                                                                                                                                                                                                                                                                             1205
                                                                                                                                                                                                                                                                                                                                                                                                           1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atggagtacgcaaagcacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gacattetegagategagtteaaaaaaggggteeetgtgaaggtgaeeaaegteaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caagcgcctccaggtctctacacgaagacccaggacccagccaaaagcccccaacacccct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaaccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                    atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                    gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                         ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggcaccacccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 caagcgcctccaggtctctacacgaagacccaggacccagccaaagccccaacacccct
                                                                                                                                                                                                                                                     gaatatcatcgtctccagagcaaggtcactgccaaatag
                                                                                                                                                                                                                                                                                                                  ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               724
```

```
δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens US-09-710-281-5043
                                                                            Qy
                                                                                                            DЬ
                                                                                                                                    Qy
                                                                                                                                                                   В
                                                                                                                                                                                            Qy
                                                                                                                                                                                                                         Вр
                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                               Вþ
                                                                                                                                                                                                                                                                                                        Ωy
                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              р
DЬ
                       Qy
                                                      멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID N
SOFTWARE: FastSEQ
SEQ ID NO 5043
LENGTH: 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                            545
                                                                                                                                                                                                                                                                                 665
                                                                                                                                                                                                                                                                                                           541
                                                                                                                                                                                                                                                                                                                                                                481
                                                                                                                                                                                                                                                                                                                                                                                                                          421
                                                                                                                                                                                                                                                                                                                                                                                                                                                      485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245
                          841
                                                                                                              845
                                                                                                                                                                    785
                                                                                                                                                                                               661
                                                                                                                                                                                                                           725
                                                                                                                                                                                                                                                     601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185
 965
                                                                                                                                       721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                  781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aaggaagacttcgaggaagccaggaagacaggcactgaagctttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                   atggagtacgcaaagcacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                          gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc
atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                         ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                                                                                                                                              gacattotogagatogagttoaaaaaaggggttocotgtgaaggtgaocaacgtoaaggat
                                                                                                                                                                                                                                      caagcgcctccaggtctctacacgaagacccaggacccagccaaagccccaacacccct
                                                                                                                                                                                                                                                                              atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                              atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                                                                      atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                            gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                   aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
             atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                   catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                        caagcgcctccaggtctctacacgaagacccaggacccagccaaagccccaacacccct
                                                                                                                                                                gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                      catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.5%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1232.6; DB 2
Pred. No. 6.1e-294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 28; Length 1656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                     540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
                                                            964
                                                                                     840
                                                                                                                 904
                                                                                                                                             780
                                                                                                                                                                         844
                                                                                                                                                                                                                              784
                                                                                                                                                                                                                                                        999
                                                                                                                                                                                                                                                                                                              600
                                                                                                                                                                                                                                                                                                                                          664
                                                                                                                                                                                                                                                                                                                                                                                                 604
                                                                                                                                                                                                                                                                                                                                                                                                                             480
                                                                                                                                                                                                                                                                                                                                                                                                                                                         544
```

```
밁
                              Ş
                                                       망
                                                                              QΥ
                                                                                                         В
                                                                                                                             δÃ
                                                                                                                                                            DЬ
                                                                                                                                                                                  Ş
                                                                                                                                                                                                           ф
                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                            Ър
                                                                                                                                                                                                                                                                             δÕ
                                                                                                                                                                                                                                                                                                                                                                           Sn
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLITIFLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.2041-001 CURRENT APPLICATION NUMBER: US/09/716,920 CURRENT FILING DATE: 2000-11-20 PRIOR REPLICATION NUMBER: 60/166,507 PRIOR FILING DATE: 1999-11-19 NUMBER OF SEQ ID NOS: 1641 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-09-716-920-1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 1235
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Fas
SEQ ID NO 1274
LENGTH: 1656
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1274, Application US/09716920 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens 09-716-920-1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
       425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1021
                                                          365
                                                                                                           305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1081
                                                                                                                                 181
                                                                                                                                                            245
                                                                                                                                                                                   121
                                                                                                                                                                                                            185
                                                                                                                                                                                                                                                             125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          901
                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                            Local Similarity
nes 1235; Conserv
             aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgcccacagga
aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                  gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                               gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                 aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                 aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                    atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 184
                                                                                                                                                                                                                                                                   atgtocagcaaaggctccgtggttctggcctacagtggcggccttggacacctcgtgcatc
                                                                                                                                                                                                     ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99tgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tcccaggagcgagtggaaagtgcaggtgtccgtcctcaagggccaggtgtacatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gtgtalaccggttlacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lloyd, Clare M.
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                      99.5%;
99.7%;
                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                    Score 1232.6; DB 2
Pred. No. 6.1e-294;
                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULES
                                                                                                                                                                                                                                                                                                                                 DB 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1239
                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                Length 1656;
                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                     Gaps
  484
                                                    424
                                                                                                     364
                                                                                                                                                                              180
                                                                                                                                                                                                       244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1020
                                                                                                                                                                                                                                                                                                      0,
                                                                                                               US-09-726-175-2581
                                                                                                                                                                                     Qy
                                                                                                                                                                                                                В
                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                       QY
                                                                                                                                                                                                                                                                                                                                                                  Ъ
                                                                                                                                                                                                                                                                                                                                                                                        Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                           δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ωy
                                                                                   Sequence 2581, Application US/09726175 GENERAL INFORMATION:
                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: NOVEL TITLE OF INVENTION: THEREFFILE REFERENCE: 1600.2054-
```

```
1325
                                                                                                         1265
                                                                                                                                                                                                                                                                         1145
                                                                                                                                                                                                                                                                                                                  1021
                                                                                                                                                                                                                                   1081
                                                                                                                                                                                                                                                                                                                                                            1085
                                                                                                                                                                                                                                                                                                                                                                                                                                             1025
                                                                                                                                                                                                                                                                                                                                                                                                   961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 785
               gaatatcatcgtctccagagcaaggtcactgccaaatag
                                                                                              ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                    ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                             ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                     ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                    accatggaccgggaagtgcgcaaaatcaaascaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                   gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                     9tgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                  accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                tcccaggagcgagtggaaagtgcaggtgtccgtcctcaagggccaggtgtacatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \verb|catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt|\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99caccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gacattetegagategagtteaaaaaaggggteeetgtgaaggtgaeeaacgteaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caagegeetecaaggtetetacaegaagaeeeeaggaeeeageeaaageeeeeeet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         caagogcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
-;
                                                                                                                                                                                   1264
                                                                                                                                                                                                                                                                  1204
                                                                                                                                                                                                                                                                                                                                                                                           1020
                                                                                                                                                                                                                                                                                                         1080
                                                                                                                                                                                                                                                                                                                                                                                                                                  1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                664
```

Gearing, David P. Fraser, Christopher C. Donovan, Michael J. Holtzman, Douglas A.

THEREFOR)0.2054-001

NUCLEIC

ACID

MOLECULES

```
; TYPE: DNA; ORGANISM: Homo sapiens US-09-726-175-2581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          뫄
 밁
                          Qy
                                                       В
                                                                                  Qy
                                                                                                                    밁
                                                                                                                                         δõ
                                                                                                                                                                            В
                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                              đ
                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/726,175
CURRENT FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/167,859
PRIOR EILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 3770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                           601
                                                                                                                                                                                                                                        665
                                                                                                                                                                                                                                                                                                605
                                                                                                                                                                                                                                                                                                                             481
                                                                                                                                                                                                                                                                                                                                                           545
                                                                                                                                                                                                                                                                                                                                                                                       421
                                                                                                                                                                                                                                                                                                                                                                                                                    485
                                                                                                                                                                                                                                                                                                                                                                                                                                                 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
 905
                                                                                                                     785
                                                                                                                                                   661
                              781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
wes 1235; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aaggaagacttcgaggaagccaggaaggaaggcactgaagcttggggccaaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctcgtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
[[]]]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aaacaaqtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgcccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                   atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacccccaagaac
                                                                                                                                                                                                                                                                                                            atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                       gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                  aaggggaacgatcaggttcgggttttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                         gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                  aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
               catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                          ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                                                                                    gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                  gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                                                             caagegeeteeaggtetetacaegaagaeeeaggaeeeaggeeaaageeeeaacaeeeet
                                                                                                                                                                                         caagegeetecaggtetetacaegaagaeeeaggaeeeageeaaageeeeeet
                                                                                                                                                                                                                                     atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                              atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                          ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1232.6; DB 29; Length 1656; Pred. No. 6.1e-294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                     420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                           480
                                                                                                                                                                                                                                                                                                                                                                                                                         544
      964
                                                               904
                                                                                                                        844
                                                                                                                                                                                  784
                                                                                                                                                                                                               660
                                                                                                                                                                                                                                           724
                                                                                                                                                                                                                                                                                                   664
                                                                                                                                                                                                                                                                                                                                540
                                                                                                                                                                                                                                                                                                                                                              604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
```

```
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.2010-001

CURRENT APPLICATION NUMBER: US/09/726,787

CURRENT FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: 60/168,132

PRIOR FILING DATE: 1999-11-30

NUMBER OF SEQ ID NOS: 3241

SOFTWARE: FastSEQ for Windows Volume 10 of Sep 10 nos: 3241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-726-787-2755
              Ş
                                              밁
                                                                         20
                                                                                                           В
                                                                                                                                     20
                                                                                                                                                                      В
                                                                                                                                                                                                Ωy
                                                                                                                                                                                                                                DЬ
                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                       US-09-726-787-2755
                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2755
LENGTH: 1656
TYPE: DNA
                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLITONAM
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              841 atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                  125
                                                                                                                                                                        185
                 241
                                                                             181
                                                                                                                                          121
                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gaatatcatcgtctccagagcaaggtcactgccaaatag 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              accatggaccgggaagtgcgcaaaatcaaaccaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag 1324
gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                            atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 184
                                                                                                                                                                                                                                                  atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                                                                                                                                                                                                                             1235;
                                                                                                      aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc 304
                                                                                                                        aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc 180
                                                                                                                                                                     ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                   ctcgtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                            Conservative
                                                                                                                                                                                                                                                                                                             99.5%;
99.7%;
                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                             Score 1232.6; DB 2
Pred. No. 6.1e-294;
                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                               DB 29; Length 1656;
                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            960
                                                                                                                                                                           244
                                                      364
                                                                                                                                                                                                                                                                                                    0
```

```
RESULT 12
US-09-726-790-2021
US-09-726-790-2021
; Sequence 2021, Application US/09726790
; GENERAL INFORMATION:
                                                                                                                                   8
                                                                                                                                                                    В
                                                                                                                                                                                            δ
                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                            р
                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              965
                                                                                                                                                                                                                                                                                                                                                                                                                                                 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
                                                                                              gaatatcatcgtctccagagcaaggtcactgccaaatag
                                                                                                                gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                    ctcggccgggagtccccactgtctctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                          ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                          99tgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                    ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                            gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                9t9tataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                        accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                          accatggaccgggaagtgcgcaaaatcaaaccaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggcaccaccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99caccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gacattetegagategagtteaaaaaaggggteeetgtgaaggtgaeegaegteaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caagegeetecaggtetetacaegaagaeeeaggaeeeaggeeaaggeeeeeageeeeet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caagegeetecaggtetetaeaegaagaeeceaggaeecageeaaageeeceaaeaeeeeet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgttggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9tcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgcccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     900
                                                                                                                                                                                                                                                                                                                 1080
                                                                                                                                                                                                                                                                                                                                                                                                          1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424
```

APPLICANT:

Williamson, Shyjan, And

Andrew W

```
Ωy
                                                                                                   В
                                                                                                                             QΥ
                                                                                                                                                              밁
                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                ρ
                                                                                                                                                                                                                                                                                 Дb
                                                                                                                                                                                                                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                    Qγ
                                                                                                                                                                                                                                                                                                                                                                                                     Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΩV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo
US-09-726-790-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 1235; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Fa
SEQ ID NO 2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL NUCLEIC ACID METHER FOR INVENTION: THEREFOR FILE REFERENCE: 1600.2021-001
CURRENT APPLICATION NUMBER: US/09/726,790
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/168,038
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 2814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                       845
            781
                                                                    721
                                                                                                   785
                                                                                                                              661
                                                                                                                                                              725
                                                                                                                                                                                          601
                                                                                                                                                                                                                        665
                                                                                                                                                                                                                                                   541
                                                                                                                                                                                                                                                                                 605
                                                                                                                                                                                                                                                                                                              481
                                                                                                                                                                                                                                                                                                                                            545
                                                                                                                                                                                                                                                                                                                                                                         421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425
                                                                                                                                                                                                                                                                                                                                                                                                       485
                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 atgtocagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                              ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                 ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                                                          gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                        gacattctcgagattcgagttcaaaaaaggggttccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                                   caagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccct
                                                                                                                                                                    caagegeetecaggtetetacaegaagaeeeaggaeeeageeaaageeeeeaeeeeet
                                                                                                                                                                                                             atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                               atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacccccaagaac
                                                                                                                                                                                                                                                                                         atggagtacgcaaagcacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                          atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                 gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                    gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                             aaggggaacgatcaggtccggtttgagctcagctgctactcactggcccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                             aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctcgtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaggaagacttcgaggaagccaggaaggcactgaagctttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOVEL NUCLEIC ACID MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1232.6; | Pred. No. 6.1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 29; Length 1656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
    840
                                                                                                                                                      784
                                                                                                                                                                                                                                             600
                                                                                                                                                                                                                                                                           664
                                                                                                                                                                                                                                                                                                                                                                 480
                                                                                                                                                                                                                                                                                                                                                                                               544
                                                                                                                                                                                                                                                                                                                                                                                                                                                           484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
```

4;

Indels

0;

Gaps

0;

```
δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      рЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/732,630
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/169,681
PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 60/171,350
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/189,315
PRIOR FILING DATE: 2000-03-14
PRIOR PRIOR APPLICATION NUMBER: US 60/203,791
PRIOR APPLICATION NUMBER: US 60/203,791
PRIOR APPLICATION NUMBER: US 60/210,600
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: US 60/220,114
PRIOR APPLICATION NUMBER: US 60/220,114
PRIOR TILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 4660
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-732-630-4186
                                                       US-09-732-630-4186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4186, Application US/09732630
                                                                                                                                                           SEQ ID NO 4186
LENGTH: 1725
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Berger, Allison
APPLICANT: Zhao, Xumei
TITLE OF INVENTION: MOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF CERVICAL CANCER
FILE REFERENCE: MRI-008B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schlegal, Robert
APPLICANT: Deeds, James
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1021
                                                                       OTHER INFORMATION: n =
                                                                                   NAME/KEY: misc_feature
LOCATION: 1,2,1725
                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1085
                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            841 atctacgagaccccagcagcaccatcctttaccattgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaaggtgtataccggtttctggccacagccctgagtgtgaatttgtccgccactgcatcgccaaggtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gaatatcatcgtctccagagcaaggtcactgccaaatag 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ctcggccgggagtccccactgtctctctctacaatgaggagctggtgagcatgaacgtgcag 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \verb|tcccaggagcgagtggaagggaaagtgcaggtgtccgtcatagggccaggtgtacatc|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berger, Allison
   99.5%;
99.7%;
                                                                         a,c,
                                                                         ģ
   Score 1232.6; DB 2 pred. No. 6.1e-294;
                  DB 29; · Length 1725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PREVENTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                        Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dр
                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                     QV
                                                                                                                                                                                                                                                                                                     망
                                                                                                                                                                                                                                                                                                                              δδ
                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                          DЬ
                                                                                                                                                   20
                                                                                                                                                                                  д
                                                                                             γΩ
         멍
                                  QΥ
                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192
                                                                                                                          1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
                                                                                                                                                                                                                                                                                                                                                               792
                                                                                                                                                                                                                                                                                                                                                                                                                          732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
```

```
132 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                    841 atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                             912 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaggaagacttcgaggaagccaggaagacagccctgaagctctggggcccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctcgtgtgggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaggaagacttcgaggaagccaggaagacgcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaggggaacgatcaggttcgggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                  catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 840
                                                                                                                                                                                                                                                                                                                                                                                                                              ggcaccaccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggcaccacccaccagaccttcttggagctcttcatgtacctgaacgaagtcgcgggcaag 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gacattotogagatogagttoaaaaaaggggtocotgtgaaggtgacoaacgtoaaggat 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         caagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              caagcgcctccaggtctctacacgaagacccaggacccagcccaaagcccccaacacccct
toccaggagcgagtggaagggaaagtgcaggtgtccgtcctcaagggccaggtgtacatc
                                                                                                      gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                  accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                           accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                       atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                  gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  671
                                                                                                                                                                                    1091
                                                                                                                                                                                                                                                                                                                                                                                                                                              911
                                                                                                                                                                                                                                                                                                                  900
                                                                                                                                                                                                                                                                         1031
                1211
```

```
Š
                                                      B
                                                                                     Qy
                                                                                                                         밁
                                                                                                                                                         Ş
                                                                                                                                                                                                В
                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                     DЬ
                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                        γ
                                                                                                                                                                                                                                                                                                                                                                                                             Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo
US-09-770-173-2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-770-173-2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Sin
Matches 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2339, Application US/09770173 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2059-001
CURRENT APPLICATION NUMBER: US/09/770,173
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,876
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 3167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: White, David APPLICANT: Pan, Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1755
                                                                                                                           491
                                                                                                                                                                                                                                                      371 gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                           191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1332 gaatatcatcgtctccagagcaaggtcactgccaaatag 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1081 ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
 atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                      gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg 480
                                   gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg 610
                                                                                                          aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 550
                                                                                                                             aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
                                                                                                                                                                               aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                      aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgcccacagga
                                                                                                                                                                                                                                                                           gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                              aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                 aaggaagacttcgaggaagccaggaagacagcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99tgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99tgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.5%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1232.6; DB 30; Length 1755; Pred. No. 6.2e-294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                   490
                                                                                                                                                                                                                                                                                                                               370
                                                                                                                                                                                                                                                                                                                                                                                                  310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                      US-09-760-475-983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ДЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  日
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ωy
                                                                                                                       SEQ ID NO 983
LENGTH: 2057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QΥ
                                                                                                                                                                                                                                                                                                     Sequence 983, Applic GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Вþ
                                                                                                                                                                        Prior application data removed - NUMBER OF SEQ ID NOS: 4122
                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/760,475
CURRENT FILING DATE: 2001-01-16
                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ49
                                                                                                                                                            SOFTWARE:
                                                                   TYPE: DNA
ORGANISM: HOMO sapiens
FEATURE:
NAME/KEY: SITE
         OTHER INFORMATION: n equals a,t,g,
                               NAME/KEY: SITE
LOCATION: (2036)
                                                                                                                                                                                                                                                                                                                                                                                                                     1201 gaatatcatcgtctccagagcsaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1271 ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1091 gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1031 accatggaccgggaagtgcgcaaaatcaaaccaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    961 gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              841 atctacgaggacccaggcaggcaccatcctttaccatgctcatttagacatcgaggccttc 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    851 ggcaccaccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       791 gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          661 gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              731 caagegeetecaggtetetacaegaagaeeeaggaeeeageeaaageeeeeaaeaeeeet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag 1140
                                                                                                                                                                                                                                                                                                                                                                                                      gaatatcatcgtctccagagcaaggtcactgccaaatag 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99tgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99Caccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Ver.
                                                                                                                                                                                                                                                                                                                  Application US/09760475
                                                                                                                                                                                     consult PALM or file wrapper
```

1090

960

1030

. 970

910

```
US:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                            δõ
                                                                                                                                                       В
                                                                                                                                                                              δÃ
                                                                                                                                                                                                           밁
                                                                                                                                                                                                                               Qy
                         Ş
                                                                         QΥ
                                                                                                     B
                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (2038)
OTHER INFORMATION:
-09-760-475-983
                                                                                                        1313
                                                                                                                                                        1253
                                                                                                                                                                                                           1193
                                                                                                                                                                                                                                                             1133
                                                                                                                                                                                                                                                                                                               1073
                                                                                                                                                                                                                                                                                                                                                                 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          713
                                                                                                                                                                                                                                                                                                                                       541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                781
                                                                                                                                                                                 721
                                                                                                                                                                                                                                   661
                                                                                                                                                                                                                                                                                     601
                                                                                                                                                                                                                                                                                                                                                                                         481
                                                                                                                                                                                                                                                                                                                                                                                                                  953
                                                                                                                                                                                                                                                                                                                                                                                                                                           421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaggaagacttcgaggaagccaggaaggactgaagcttgaggctcgaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgcccacagga
                                                                                                                                                                                                                                                          atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                                                        atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac 600
                                                                                                                                                                                                                                                                                                                                                             atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc 1072
                                                                                                                                                                                                                                                                                                                                                                            atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc 540
                                                                                                                                                                                                                                                                                                                                                                                                                  gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                              gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgccacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                     ggcaccacccaccagaccttccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                        gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat 1252
                                                                                                                                                                                                                     gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat 720
                                                                                                                   catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 840
                                                                                                                                                       ggcaccaccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                  atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                      catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n equals a,t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1232.6; DB 3
Pred. No. 6.4e-294;
9; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or
P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 30; Length 2057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                       1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              772
      1492
                                                        1432
                                                                                                          1372
                                                                                                                                                             1312
                                                                                                                                                                                     780
                                                                                                                                                                                                                                                                                                                 1132
                                960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
```

밁

```
QΥ
                                                                                                                                                                                                                                                                                                 망
                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                Db
                                                                                                                                                                                 Qy
                                                                                                                                                                                                                        뫄
                                                                       В
                                                                                                        QΥ
                                                                                                                                                                                                                                                                                                 1493
                                                                                                            1141
                                                                                                                                                  1613
                                                                                                                                                                                                                                                             1021
                                                                                                                                                                                                                                         toccadgagcgagtggaagggaaagtgcaggtgtccgtcctcaagggccaggtgtacatc
                                                                                                                                                                                                                                                                                             gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                 gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                 gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                       ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                            ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                  ctcggccgggagtccccactgtctctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                      tcccaggagcgagtggaaagtgcaggtgtccgtcctcaagggccaggtgtacatc
gaatatcatcgtctccagagcaaggtcactgccaaatag
                                                                                                                                                ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                          1672
                                                                                                                                                                                                                                 1612
```

Search cor Job time: completed: February ne: 6091 sec 12, 2002, 14:27:58

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1199.6
1183.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pending_Patents_NA_New:*

1: //gqn2_6/ptodata/2/pna/ptodata/2/pna/ptodata/2/pna/li

3: //gqn2_6/ptodata/2/pna/li

4: //gqn2_6/ptodata/2/pna/li

5: //gqn2_6/ptodata/2/pna/li

6: //gqn2_6/ptodata/2/pna/li

6: //gqn2_6/ptodata/2/pna/li

9: //gqn2_6/ptodata/2/pna/li

9: //gqn2_6/ptodata/2/pna/li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    February 12, 2002, 13:10:07; Search time 4918.34 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 atgtccagcaaaggctccgt.....gcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-775-693-1
1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2043436 seqs, 1186999438 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match
                                                                           999.4

444.0

999.6

440.5

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

440.6

44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq: *
/cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq: *
/cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq: *
/cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq: *
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq: *
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq: *
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq: *
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq: *
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq: *
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq: *
/cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1571
1828
2004
2005
1871
987
S US-09-981-353-86
S US-09-898-888A-13594
US-60-340-187-216
US-60-340-187-330
US-60-340-187-951
S US-09-998-598-291
S US-09-998-598-707
US-09-998-598-707
US-09-998-598-787
US-09-998-598-787
US-09-998-598-787
US-09-933-524A-54674
US-09-933-524A-54674
US-09-933-524A-54673
US-09-933-524A-63203
US-09-933-524A-63203
US-09-933-524A-63203
US-09-933-524A-34673
US-09-933-524A-34673
US-09-933-524A-3480-2266
US-09-933-524A-63203
US-09-933-524A-63203
US-09-933-524A-63203
US-09-933-524A-63203
US-09-933-524A-63203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΙD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (without alignments)
598.044 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 2701, App Sequence 951, Apr Sequence 2701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                   951, App
467, App
702, App
907, App
1365, Ap
1787, App
1365, Ap
1787, App
1787, App
1787, App
1787, App
1787, App
1787, App
1786, App
1786, App
1786, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86, Appl
13594, A
```

o

499.8 467.4 457.4

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence

883, APP 19540, A 54673, A 2065, A 22065, A 38994, A 1772, AP 22593, A

Sequence

8 9 10 11 12 13

O a

453.2 453.2 453.2 434.

ი

421.8 405.4 404.8

US-10-029-386-22593

Sequence Sequence Sequence Sequence

18 19 20 21 22 23 23

Qу Дь Qу	Oy Oy Db	Que Bes Mat Qy Db	US-09- J Sequ J Sequ J Sequ J Sequ J Sequ J Sequ J TIT	25 25 27 27 27 27 27 27 27 27 27 27 27 27 27
241 gca 329 gca 301 aaa	21 aag 09 aag 81 att 69 att	ry Match t Local S ches 1234 1 atgt 1	SULT 1 -09-981-353-E Sequence 86, Sequence 86, APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: INTIE OF INI CURRENT APPLICANT: INDIA ORGANISM: FEATURE: ANAE/KEY: ANA	403 397 389.8 389.8 384.8 384.8 382.6 376.6 376.6 371.4 371.4 371.4 354.4 352.2 352.2 352.2 353.2 359.8
ctgtatga ctgtatga caagtgga	aagactt	imilarit; Conse; Conse; Conse; IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Application/MATION: WAGTION WAGTION Jones, in	332.11 321.15 31.09 30.99 30.99 30.69 30 30.69 30 30 30 30 30 30 30 30 30 30 30 30 30
ggaccy ggaccy	gagga: agga: agcag	y 99 rvativ ggctcc ggctcc aaggaa	on US W. W. Vid I ENES 38 US 0MBEI 200: 194 m	391 4429 4435 4435 4403 4403 4403 459 4459 3468 3594 3594 3594 3594
cta cta	gc 	. 4: e e e e e e e e e e e e e e e e e e e	7 to 18 to 2	766757776677657876667
	caggaagaaggactgaagcttggg	; Score 1231; DB 6; I ; Pred. No. 0; ; Pred. No. 0; ; O; Mismatches 5; gttctggcctacagtggcggcctg [)9981353 KPRESSED IN COLON CANCER US/09/981,353 10-11	US-09-925-564-28045 US-09-937-875A-6305 US-09-933-524A-49321 US-09-933-524A-6820 US-09-933-554A-18820 US-09-939-397-1771 US-09-939-397-1771 US-09-933-524A-92776 US-09-935-564-28304 US-09-975-640A-11846 US-09-975-640A-11846 US-09-925-564-28986 US-09-925-564-28986 US-09-925-564-280735 US-09-925-564-280735 US-09-925-564-280735 US-09-925-564-280735 US-09-925-5640A-26735 US-09-975-640A-26735 US-09-975-640A-26735 US-09-975-640A-26735 US-09-975-640A-26735 US-09-975-640A-26735 US-09-975-640A-26735 US-09-975-640A-26735
	ccaaaagytytte 10	th 1571; els 0; Gar acctcgtgcatc (acctcgtgcatc (acctcgtgcatc (acctcgtgcatc (accatcgtgcatc (accatcgtgcatc (accatcgtgcatc (accatcgtgcatc (accatcgtgcatc)		Sequence 28045, Ap Sequence 49321, Ap Sequence 58820, Ap Sequence 6718, Ap Sequence 1771, App Sequence 1771, App Sequence 28304, A Sequence 11846, A Sequence 11846, A Sequence 28044, A Sequence 28044, A Sequence 28044, A Sequence 21043, A Sequence 27043, A Sequence 27043, A Sequence 27043, A Sequence 27035, A Sequence 2735, A

0;

```
US-09-898-888A-13594
                                                                                                                                                                                                                     ν
                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                  Ъ
                                                                                                                                                                                                                                                                                                                                              γ
                                                                                                                                                                                                                                                                                                                                                                               DЬ
                                                                                                                                                                                                                                                                                                                                                                                                           δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Дb
                                                                                             Sequence 13594, Application US/098988888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
           APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-748CON1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
CURRENT APPLICATION NUMBER: US/09/898,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              рЬ
                                                                                                                                                                                          1201 gaatatcategteteceagageaaggteaetgeeaaatag 1239
                                                                                                                                                                                                                                                1141 ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                                                                                                               1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569 atggagtacgcaaagcaacatgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389
                                                                                                                                                                          gaatatcatcgtctccagagcaaggtcactgccaaatag
                                                                                                                                                                                                                                  99tgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
                                                                                                                                                                                                                                                                                             ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                          919tataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                            gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       accatggaccgggaagtgcgcaaaatcaaaccaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \verb|catggcgtgggcgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99caccacccacccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggcaccacccaccagacotccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gacattotogagatogagttoaaaaaaggggtocotgtgaaggtgacoaacgtoaaggat 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caagegeetecaggtetetacaegaagaeeecaggaeeecageeaageeeecaaeaeeeeet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9tcattgctccctggaggatgcctgaattctacaaccggttcaaggggccgcaatgacctg 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1048
                                                                                                                                                                                                                                                                                                                                                               1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       688
```

```
g
                                               QΥ
                                                                               DЬ
                                                                                                            οy
                                                                                                                                              Вþ
                                                                                                                                                                           δÃ
                                                                                                                                                                                                           Ър
                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                     29
                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                 QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q_{\overline{Y}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: n = A, T, C US-09-898-888A-13594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/205,070
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 45207
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 13594
LENGTH: 1828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/340,623
PRIOR FILING DATE: 1999-06-28
                796
                                               718
                                                                              658 cotgacattotogagatogagttoaaaaaaggggtocotgtgaaggtgaccaacgtcaag 717
                                                                                                                           676 aaccaagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacc
                                                                                                                                           598 aaccaagcgcctccaggtctctacacgaagacccaggacccagccaaagccccaacacc
                                                                                                                                                                                                           616
                                                                                                                                                                                                                                                                        556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: (1)...(1828)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                     496
                                                                                                                                                                                                                                                                                                                                                                    419
                                                                                                                                                                                                                                                                                                                                                                                 436 gaaaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataa
                                                                                                                                                                                                                                                                                                                                                                                                                                 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 aaggaagacttcgaggaagccaggaaggaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
               gatggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggc
gatggcaccaccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggc
                                                           cctgacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                          agcatggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaag
                                                                                                                                                                                                         agcatggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaag
                                                                                                                                                                                                                                                       Lgatggagtacggcaaagcaacacgggattcccatcccggtcactcccaagaacccgtgg
                                                                                                                                                                                                                                                                                                                   aggtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacc
                                                                                                                                                                                                                                                                        tgatggagtac-gcaaagcacacgggattccccatcccggtcactcccaagaacccgtgg
                                                                                                                                                                                                                                                                                                                                                                                                 gaaaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataa 418
                                                                                                                                                                                                                                                                                                                                       aggtcattgctccctggaggatgcctgaattctacaaccggttcaaggggccgcaatgacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                               | caaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccac-ggcgccacag
                                                                                                                                                                                                                                                                                                                                                                                                                                             caaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacgggcgccacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gcactgtatgaggaccgctacctcctgggcacctctcttgccagggccctgcatcgcccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcactytatyaggaccyctacctcctgggcacctctctttgcca-ggccctgcatcgccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atytocagcaaaggotocgtggttotggootacagtggoggootggacacotogtgoato 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1199.6;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω,.
```

255

435

795

855

Gaps

Ψ

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-60-340-187-216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 216, Applica GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                PRIOR AFFLICATION NUMBER: US 09/552,317
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR APPLICATION NUMBER: PCT/US00/35017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Jian-I
                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/60/340,187
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 09/488,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                   PRIOR
                                                                                                                                                                                                                                                                                            PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                        PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                            PRIOR
                                                                                                                                                                                 PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1276 aaggaatatcatcgtctccagagcaaggtcactgccaaatag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aagcatggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccga 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aagcatggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccga 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ttcaccatggaccgggaagtgcgcaaaatcaaaccaaggcctgggcttgaaatttgctgag
                                                                                                                        APPLICATION NUMBER: PCT/US01/03800 FILING DATE: 2001-02-05
                                                                                                                                                            APPLICATION NUMBER: US 09/560,875
FILING DATE: 2000-04-27
                                                                                                                                                                                                 APPLICATION NUMBER: US 09/496,914 FILING DATE: 2000-02-03
                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT, FILING DATE: 2001-01-25
                                                                                                                                                                                                                                                                          FILING DATE: 2000-12-22
APPLICATION NUMBER: US 09/491,404
FILING DATE: 2000-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaggaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cagggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cagggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atcctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atcctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtg 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctggtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgcc 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctggtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgcc 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttcaccatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgag
             APPLICATION NUMBER: US 09/577,409
FILING DATE: 2000-05-18
APPLICATION NUMBER: PCT/US01/04927
FILING DATE: 2001-02-26
                                                                                                      APPLICATION NUMBER: US 09/515,126
                                                                                      FILING DATE: 2000-02-28
APPLICATION NUMBER: US 09/519,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang, Zhiwei
Wang, Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ghosh, Malabika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boyle, Bryan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weng, Gezhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/60340187
                                                                                                                                                                                                                                                          PCT/US01/02623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1035
```

```
; NAME/KEY: CDS
; LOCATION: (95)..(346)
US-60-340-187-216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                   QУ
                                                                                                                                                                                                                                                                                          Вþ
                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db
                                                                                                                                              В
                                                                                                                                                                              QΥ
                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 216
LENGTH: 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2000-05-19 PRIOR APPLICATION NUMBER: PCT, PRIOR FILING DATE: 2001-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 1188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/US01/08656
PRIOR FILING DATE: 2001-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/649,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/US01/08631 PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT, PRIOR FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR EILING DATE: 2000-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 1192
SOFTWARE: pt_FL_genes Version 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 540
                                                                                                                                                                                                                                                                                                                                                                   661
                                                                                                                                                                                                                                                                                                                                                                                  601
                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 aaggaagacttcgaggaagccaggaaggaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                            721
                                                                                                                                                                                                                                                                                                                              241
961 atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                   481 atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                             421
                                                                                                                                                             361 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
                                                                                                                                                                                                               781 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ctcgtgtgggctgaaggaacaaggctatgacgtcattggcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-05-18
APPLICATION NUMBER: PCT/US01/14827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/552,929 FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/770,160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                    aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                        gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                                                           gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc 300
                                                                                                                                                                                                                                                                                                                                                               aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                    aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccaccggcgccacagga 360
                                                                     gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                        gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.5%;
99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT/US01/04941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09/540,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09/574,454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1183.8;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
```

Gaps

0;

600

```
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: DCT/US01/404
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 330 Application
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Jian-Ru
APPLICANT: Wang, Jian-Ru
APPLICANT: Wang, Gezhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-60-340-187-330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                     APPLICANT: Boyle, Bryan J
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 813
                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/60/340,187 CURRENT FILING DATE: 2001-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1141 ggtgattatgagccaactgatgccaccgggttcatcaactcaattccctccaggc 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1561 ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1621 ggtgattatgagccaactgatgccaccgggttcatcaacatcaaattcctcagcc 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1321 atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1261 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1201 ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1141 gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               961 gtgtataccggtttacggcctagccctgggtgtgaatttgtccgccactgcatcgccaag 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1081 caagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccct 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1021 atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       841 atctacgagaccccagcaggcaccattcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       781 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661 gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601 caagcgcctccaggtctctacacgaagacccaggacccaggccaaagcccccaacacccct 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541 atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac 600
FILING DATE:
           APPLICATION NUMBER: US 09/496,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         teceaggagegagtggaagggaaagtgeaggtgteegteeteaagggeeaggtgtaeate 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99Caccaccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag 780
                                                                                                                                                                                                                                                                                                                                                                                    Wang, Zhiwei
Wang, Jian-Rui
Ghosh, Malabika
Weng, Gezhi
Boyle, Bryan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/60340187
2000-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1620
```

```
B
                                                                                                                                                                   δÃ
                                                                                                                                                                                                           Ъ
                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                 γ
                                                                                                                                                                                                                                                                                                                                                                Db
                                                                                                                                                                                                                                                                                                                                                                                                                                         DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-60-340-187-330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 1188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: pt_FL_genes Version 6.0 SEQ_ID_NO 330_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2005
TYPE: DNA
ORGANISM: Homo:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 201 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (254)..(2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US01/04941
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION UNMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US01/04927 PRIOR FILING DATE: 2001-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-03-07 PRIOR APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/519,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/577,409 PRIOR FILING DATE: 2000-05-18
361 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
                                    782 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga 841
                                                          301 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga 360
                                                                                                                722 gcactgtatgaggaccgctacctcctgggcacctctctttgccaggccctgcatcgcccgc
                                                                                                                                                                                                           662
                                                                                                                                                                                                               602
                                                                                                                                                                                                                                                                                          121 aaggaagacttcgaggaagccaggaaggcactgaagctttggggccaaaaaggtgttc 180
                                                                                                                                                                                                                                                                                                                                              542 ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                       482 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 541
                                                                                                                                                                                                                                                                                                                                                                61 ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/08656 FILING DATE: 2001-04-18 APPLICATION NUMBER: US 09/577,408 FILING DATE: 2000-05-18
                                                                                                                                                                                           gcactgtatgaggaccgctacctcctgggcacctctctttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                                                                    aaggaagacttogaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/14827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/770,160 FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/08631
FILING DATE: 2001-03-30
APPLICATION NUMBER: US 09/552,929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/649,167 FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/574,454 FILING DATE: 2000-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US FILING DATE: 2000-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/03800 FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/560,875 FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1183.8;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09/515,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; Length 2005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
```

Gaps

0,

601

781

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ДЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вb
                                                                                                                                                                   ; Sequence 951, Application GENERAL INFORMATION: APPLICANT: Tang, Y. Tom APPLICANT: Wang, Zhiwei APPLICANT: Wang, Jian Ru
                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                           US-60-340-187-951
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids ar
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 813
CURRENT APPLICATION NUMBER: US/60/340,187
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 09/488,725
                                                                                                                      APPLICANT:
                                                                                                                                    APPLICANT:
                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   842
                                                                                                                                                                                                                                                                                                                               1622
                                                                                                                                                                                                                                                                                                                                                                                                                                1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atggagtacgcaaagcaacacgggattccccatcccggtcactcccaagaaccccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gacattctcgagatcgagttcaaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggcaccacccacacacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccct
                                                                                                                                                                                                                                                                                                                                            ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggc 1195
                                                                                                                                                                                                                                                                                                                                                                                                              ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          accatggaccgggaagtgcgcaaaatcaaaccaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggcaccaccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggtgattatgagccaactgatgccaccgggttcatcaacatcaaattcctcagcc
                                                                                                                                                                                                                                                                                                                                                                                              ctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gtgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        accatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang, Zhiwei
Wang, Jian-Rui
Ghosh, Malabika
Weng, Gezhi
Boyle, Bryan J
                                                                                                                                                                                                                                           Application US/60340187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             660
                                                                                                                                                                                                                                                                                                                                                                                                    1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1080
```

```
PEATURE:

NAME/KBY: misc_feature

LOCATION: (1)...(1871)

OTHER INFORMATION: n =

US-60-340-187-951
                                                                                               밁
                                                                                                                         Qy
                                                                                                                                                         Дb
                                  Дb
                                                             Qγ
                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: pt_FL_genes Version 6.0
SEO ID NO 951
SEO ID NO 951
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                       Matches 1044;
                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR
                                  121
                                                                121
                                                                                               61
                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-02-20
APPLICATION NUMBER: US 09/577,409
APPLICATION NUMBER: US 09/577,409
APPLICATION NUMBER: 2000-05-18
APPLICATION NUMBER: 2000-05-18
                                                                                                                                                         ш
                                                                                                                                                                        1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US00/35017 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/08656
FILING DATE: 2001-04-18
APPLICATION NUMBER: US 09/577,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-03-31
APPLICATION NUMBER: US 09/649,167
FILING DATE: 2000-08-23
APPLICATION NUMBER: PCT/US01/08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2001-02-05
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US
FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/02623 FILING DATE: 2001-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/04941 FILING DATE: 2001-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/574,454 FILING DATE: 2000-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 09/519,705 FILING DATE: 2000-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-05-18
APPLICATION NUMBER: PCT/US01/04927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/03800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/770,160 FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/14827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 09/552,929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 09/540,217
                                                                                                                                                      atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
ctcgtqtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc
                                                                                         ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                  aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-05-16
                                                                                                                                                                                                                                      60.0%;
87.9%;
                                                                                                                                                                                                                                                                                                                  a,t,c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 09/552,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09/496,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09/491,404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09/515,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09/560,875
                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                    Score 742.8; DB y;
Pred. No. 5.9e-194;
                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                    Length 1871;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                            37;
```

δã

181

180 180 Gaps

20;

```
밁
                                Ş
                                                            밁
                                                                                     Š
                                                                                                                  В
                                                                                                                                             Qγ
                                                                                                                                                                          ď
                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                          DЬ
                                                                                                                                                                                                                                                                                                                 ρ
                                                                                                                                                                                                                                                                                                                                                Ъ
                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
       1141
                                                                                                                                                                                                                                                                                          841
                                                                                                                                                                                                                                  901
                                                                                                                                                                                                                                                                                                                    824
                                                                                                                                                                                                                                                                                                                                                781
                                                                                                                                                                                                                                                                                                                                                                                                                                                             661
                                                                                                                                                                                                                                                                                                                                                                           770
                                                                                                                                                                                                                                                                                                                                                                                                       721
                                                                                                                                                                                                                                                                                                                                                                                                                                 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                          tctctacaatgaggagctggtgagcatgaacgtgcagggtgattatga 1151
                                                                                                            gaattggtcggcccttgccttcgccaaagtccccaggagcgagtggaaggggaaaagtgca
tctctctacaatgaaggagctggtgaagcatggaacgtgccagggtga
                                                      ggtgtcccgtccctcaaagggcccaggtgtacatccctcggcccggaagtcccccactgt
                                                                     ggtgtccgtcctc----aagggccaggtgtacatcc--tcggccgggagtccccactgtc
                                                                                                                          gaatttgtccgccactgcat---cgccaagtcccaggagcgagtggaaggg-aaagtgca
                                                                                                                                                                   ctgggctttgaatttgttgagcttggtgtataccggttttctggcacagcccctgagtgt
                                                                                                                                                                                   ctgggcttgaaatttgctgagc-tggtgtataccggtttac--ggcctagccctgagtgt
                                                                                                                                                                                                                                                                                 gaatgaagtcccgaggtatct----acgagaccccagcaggcaccatcctttaccatgct
                                                                                                                                                                                                                           catttagacatcgaggccttcaccatgggcgggatagggcgcaaataccaaaccagggt
                                                                                                                                                                                                                                           catttagacatcgaggccttcaccatggaccgggaagtgcgcaaaatc---aaacaaggc
                                                                                                                                                                                                                                                                                                                                                        tcgcgggcaagcatggcgtgggcc--gtattgacatcgt-ggagaaccgcttcatt---g
                                                                                                                                                                                                                                                                                                                                                                                               tcaaggatgggcaccacccaccagacctttcttggagctctttcatgtacctgaacgaag
                                                                                                                                                                                                                                                                                                                                                                                                              --caaggatggcaccacccaccagacc-tccttggagctc-ttcatgtacctgaacgaag 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccctgacattctcgagatcgagtttcaaaaaaggggtccctgtggaaggtggaccaacgt 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CCCtgacattctcgagatcgag-ttcaaaaaaggggtccctgtg--aaggtgaccaacgt 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gaaccaagcgcctccaggtctctacacgaagacccaggacccagccaaagccccaacac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gagcatggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaggtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gaaaggggaacgatcaggtccggtttgagctcagctgctactcactggcccccccagata
                                                                                                                                                                                                                                                                                                                                         tcgcgggcaagcatggcgttgggccgtatttgacatcgtgggagaaccgctttcattggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gaaccaagcgcctccaggtctctacacgaagacccaggacccagccaaagccccaacac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gagcatggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aaggtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gaaaggggaacgatcaggtccggtttgagctcagctgctactcactgg-ccccccagata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caaacaagtggaaattcgcccagcgggaggggccaagtatgtgtcccacggcgccacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gcactgtatgaggaccgctacctcctgggcacc-tctcttgccaggccctgcatcgcccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caaacaagtggaaa·tcgcccagcgggagggggccaagtatgtgtcccacggcgccacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gcactgtatgaggaccgctacctcctgggcacctttttttgccaggccctgcatcgcccg
                                                                                                                                                                                                                                                                                   900
                                                                                                                                                                      1020
                                                                                                                                                                                                  993
                                                                                                                                                                                                                              960
                                                                                                                                                                                                                                                                                                              879
                                                                                                                                                                                                                                                                                                                                                                     823
                                                                                                                                                                                                                                                                                                                                          840
                                                                                                                                                                                                                                                                                                                                                                                                 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299
```

US-09-898-888A-22919

σ

Sequence 22919, Application GENERAL INFORMATION: APPLICANT: Hyseq, Inc.

US/09898888A

```
Ş
                                                                                             δÃ
                                                                  В
                                                                                                                              밁
                                                                                                                                                      Ωy
                                                                                                                                                                                       В
                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                   DЬ
                                                                                                                                                                                                                                                                           Ωy
                                                                                                                                                                                                                                                                                                              Дb
                                                                                                                                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                                                                                                                                                                     ρy
                                                                                                                                                                                                                                                                                                                                                                          Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; LOCATION: (1)...(987)
; OTHER INFORMATION: n = A,T,C
US-09-898-888A-22919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local s
Matches 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 22919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-748CON1
CURRENT APPLICATION NUMBER: US/09/898,888A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/340,623
PRIOR FILING DATE: 1999-06-28
PRIOR FILING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: US/09/205,070
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 45207
SOFTWARE: FASESEQ for Windows Version 3.0
                                    1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                           1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
       569
                                                                                                                                                                                         398
                                                                                                                                                                                                                                                   375
                                                                                                                                                                                                                                                                                 893
                                                                                                                                                                                                                                                                                                               315
                                                                                                                                                                                                                                                                                                                                             833
                                                                                                                                                                                                                                                                                                                                                                          255
                                                                                                                                                                                                                                                                                                                                                                                                                                      199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
acgtgcagggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctca
            acgtgcagggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctca
                                                                                                                                      tgtacatcctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatga
                                                                          tgtacatcctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatga
                                                                                                                     ctgagctggtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgca 1012
                                                                                                                                                                                                                                                                 aggccttcaccatggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | CCAAGAACCAAGCGCCTCCAGGTCCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCA
                                                                                                                                                                                                                                                aggccttcaccatggaccgggaa-----
                                                                                                                                                                                                                                                                                                       cccgaggtatctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcg
                                                                                                                                                                                                                                                                                                                         cccgaggtatctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcg
                                                                                                                                                                                                                                                                                                                                                                                   c999caa9catg9c9t9g9cc9tatt9acatc9tg9a9aacc9cttcattg9aatgaagt
                                                                                                                                                                                                                                                                                                                                                                                                                                            tcaaggatggcaccaccaccagacctccttggagctcttcatgtacctgaacgaagtcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atgacctgatggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atgacctgatggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacc
                                                                                                                                                                                                                                                                                                                                                                   cgggcaagcatggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acacccctgacattctc----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acacccctgacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytygaycatygatyagaacctcatycacatcayctacyayyctygaatcctygayaacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgtggagcatggatgagaacctcatgcacatcagctacgaggctggaatcctggagaacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              -ggatggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                  tgtataccggtttctggcacagccctgagtgtgaatttgtccgccactgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.8%;
87.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 554.6; DB 6;
Pred. No. 2.6e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                               1192
                                                                                                                                                      1072
                                                                                                                                                                                    448
                                                            568
                                                                                                                                                                                                                                                                              952
                                                                                                                                                                                                                                                                                                                                                                                                  832
                                                                                                                                                                                                                                                                                                                                                                                                                                                              772
                                                                                                                                                                                                                                                397
                                                                                                                                                                                                                                                                                                           374
                                                                                                                                                                                                                                                                                                                                       892
                                                                                                                                                                                                                                                                                                                                                                   314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   652
                                                                                                                                                                                                                                                                                                                                                                                                                                254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
```

```
RESULT 7
US-09-998-598-467/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens US-09-998-598-467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Вb
                                                                                                                                                                        B
                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                      QY
                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                           뮹
                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                     Q
                                                                                                                                   Qγ
                                     밁
                                                                                                      Дb
õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 467, Application GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stolk, APPLICANT: Xu, Ji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1193 ggctgaaggaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 otgotactcactggccccccagataaaggtcattgctccctggaggatgcctgaattcta 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  543 YTGCTACTCACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTA 484
                                                                                                                                                                                                                                                                                                             303
                                                                                                                                                                                                                                                                                                                                               633
                                                                                                                                                                                                                                                                                                                                                                               363
                                                                                                                                                                                                                                                                                                                                                                                                               573
                                                                                                                                                                                                                                                                            693
        933
                                                                                                          123
                                                                                                                                                                            183
                                        63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggctgaaggaatatcatcgtctccagagcaaggtcactgccaaatag 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caaccggttcaagggccgcaatgacctgatggagtacgcaaagcaacacgggattcccat 512
                                                                                                                                                                                                                                                                                                                                                                                               ggctggaatcctggagaaccccaagaacccaagcgcctccaggtctctacacgaagaccca
                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCGGTCACTCCCAAGAACCCCGTGGAGCATGGATGAGAACCTCATGCACCATCAGCTACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cccggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcagctacga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCCAT 424
                                                                                                                                                                                                                                          GGACCCAGCCAAAGCCCCCAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGT
                                                                                                                                                                                                                                                                                                                                                                               GGCTGGAATCCTGGAGAACCCCAAAAACCAAGCGCCTCCAGGTCTCTACACGAAGACCCCA
       agg 935
                                       CCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAATCAAACA 4
                                                                                                        CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAGCAGGCACCATCCTTTA 64
                                                                                                                          ccgcttcattggaatgaagtcccgaggtatctacgagaccccagcaggcaccatccttta 872
                                                                                                                                                                                          catgtacctgaacgaagtcgogggcaagcatggcgtgggcggtattgacatcgtggagaa 812
                                                                                                                                                                                                                                                                                                                             ggacccagccaaagccoccaacacccctgacattctcgagatcgagttcaaaaaaggggt
                                                        ccatgctcatttagacatcgaggccttcaccatggaccgggaagtgcgcaaaatcaaaca 932
                                                                                                                                                                            CATGTACCTGAACGAAGTCGCGGGCAAGCATCGCGTGGGCCGTATTGACATCGTGGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              John A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.7%; 99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                us/09998598

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 541; DB 7;
Pred. No. 1.2e-138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572
                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                                                   244
                                                                                                                                                                                                                                                                                                                                                    692
                                                                                                                                                                                                                                                                                                                                                                                      304
                                                                                                                                                                                                                                                                                                                                                                                                                                                      364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
```

```
LENGTH: 503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 702, Applic ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-998-598-702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δõ
                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 210121.561
CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 702
                                                                                                                                                                                                                                           Дb
                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                          US-09-998-598-907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                    Sequence 907, Application US/09998598 GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               453 caaccggttcaagggccgcaatgacctgatggagtacgcaaagcaacacgggattcccat 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 ctgctactcactggccccccagataaaggtcattgctccctggaggatgcctgaattcta 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513
                                                                                                                                                                                                                                                                                                                           421
                                                                                                                                                                                                                                                                                                                                                                                                      361 catgtacctgaacgaagtcgcgggcaagcatggcgtgggccgtattgacatcgtggagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                              753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                           481 ccatgctcatttagacatcgagg
                                                                                                                                                                                                                                                                                 873 ccatgctcatttagacatcgagg 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ctgctactcactggccccccagataaaggtcattgctccctggaggatgcctgaattcta 60
                                                                                                                                                                                                                                                                                                                     ccgcttcattggaatgaagtcccgaggtatctacgagaccccagcaggcaccatccttta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccctgtgaaggtgaccaacgtcaaggatggcaccaccaccagacctccttggagctctt 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggctggaatcctggagaaccccaagaaccaagcgcctccaggtctctacacgaagaccca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cccggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcagctacga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cccggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcagctacga 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caaccggttcaagggccgcaatgacctgatggagtacgcaaagcaacacgggattcccat 120
                                                                                                                                                                                                                                                                                                                                                                                                                           catgtacctgaacgaagtcgcgggcaagcatggcgtgggccgtattgacatcgtggagaa 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggacccagccaaagccccaacacccctgacattctcgagatcgagttcaaaaaaggggt 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggacccagccaaagcccccaacacccctgacattctcgagattcgagttcaaaaaaggggt 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggctggaatcctggagaaccccaagaaccaagcgcctccaggtctctacacgaagaccca 632
                                                                                                                                                                                                                                                                                                                                            cogetteattggaatgaagteeegaggtatetacgaggaceecageaggeaceateettta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccctgtgaaggtgaccaacgtcaaggatggcaccaccaccagacctccttggagctctt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 40.6%; Score 503; DB 7; L
Similarity 100.0%; Pred. No. 3.2e-128;
O: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09998598
                                                                                                                                                                                                                                                 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                  420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
```

```
; ORGANISM: Homo sapiens US-09-998-598-924
                                                                                                                                                                                                                                                                                                          US-09-998-598-924
                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-907
                                                                                                                                              Sequence 924, Application US/09998598
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: V. Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                         NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 924
                                                                                                             CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 210121.561
CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: COTIXA Invention Disclosure Database
SEQ ID NO 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 40.6%; Score 503; DB 7; L
Best Local Similarity 100.0%; Pred. No. 3.2e-128;
                                  TYPE: DNA
                                                  LENGTH: 503
                                                                                                                                                                                                                                                                                                                                                                       481 ccatgctcatttagacatcgagg 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 catgtacctgaacgaagtcgcgggcaagcatggcgtgggccgtattgacatcgtggagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 ctgctactcactggccccccagataaaggtcattgctccctggaggatgcctgaattcta 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                           ccatgctcatttagacatcgagg 895
                                                                                                                                                                                                                                                                                                                                                                                                                                  ccgcttcattggaatgaagtcccgaggtatctacgagaccccagcaggcaccatccttta
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccgcttcattggaatgaagtcccgaggtatctacgaggaccccagcaggcaccattcttta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           catgtacctgaacgaagtcgcgggcaagcatggcgtgggccgtattgacatcgtggagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggacccagccaaagcccccaacacccctgacattctcgagatcgagttcaaaaaaggggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99acccagccaaagcccccaacacccctgacattctcgagattcgagttcaaaaaaggggt 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggctggaatcctggagaacccaagaaccaagcgcctccaggtctctacacgaagaccca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99ct9gaatcctggagaaccccaagaaccaagcgcctccaggtctctacacgaagaccca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cccggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcagctacga 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caaccggttcaagggccgcaatgacctgatggagtacgcaaagcaacacgggattcccat 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caaccggttcaagggccgcaatgacctgatggagtacgcaaagcaacacggggattcccat 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cccggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcagctacga 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctgctactcactggccccccagataaaggtcattgctccctggaggatgcctgaattcta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        872
                                                                                                                                                                                                                                                                                                                                                                                                                                          480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
```

```
US-09-998-598-1365
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1365, Application
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-998-598-1365/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δδ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                  SOFTWARE: Corixa Invention Disclosure Database SEQ ID NO 1365
LENGTH: 503
                                                               Matches 501;
                                                                                                                                                                                                                                                                                                         APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561
                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Stolk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 503; Conserv
                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
393 ctgctactcactggccccccagataaaggtcattgctccctggaggatgcctgaattcta 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 ccatgctcatttagacatcgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 ccgcttcattggaatgaagtcccgaggtatctacgagaccccagcaggcaccatccttta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              873 ccatgctcatttagacatcgagg 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 catgtacctgaacgaagtcgcgggcaagcatggcgtgggccgtattgacatcgtggagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                753 catgtacctgaacgaagtcgcgggcaagcatggcgtgggccgtattgacatcgtggagaa 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ggacccagccaaagcccccaacacccctgacattctcgagatcgagttcaaaaaaggggt 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                573 ggctggaatcctggagaaccccaagaaccaagcgcctccaggtctctacacgaagaccca 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     513 cccggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcaggtacga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          453 caaccggttcaagggccgcaatgacctgatggagtacgcaaagcaacacgggattcccat 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393 otgotactcactggccccccagataaaggtcattgctccctggaggatgcctgaattcta 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 caaccggttcaagggccgcaatgacctgatggagtacgcaaagcaacacgggattcccat 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ctgctactcactggcccccagataaaggtcattgctccctggaggatgcctgaattcta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99acccagccaaagcccccaacacccctgacattctcgagattcgagttcaaaaaaggggt 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccctgtgaaggtgaccaacgtcaaggatggcaccaccaccagacctccttggagctctt 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggctggaatcctggagaaccccaagaaccaagcgcctccaggtctctacacgaagaccca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cccggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcagctacga 180
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      John A
                                                                         40.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Preu. ...
rive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.6%; Score 503; DB 7; L
100.0%; Pred. No. 3.2e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/09998598
                                                        Score 499.8; DB 7;
Pred. No. 2.4e-127;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 503;
                                                                                        Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572
                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
```

g

CTGCTACTCACTGGCCCCCAGATAAAGGTCATTGCTCTCTGGAGGATGCCTGAATTCTA 444

```
οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΩV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 787, Applic
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-998-598-787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-787
                                                                                                                                                               QΥ
                                                                                                                                                                                                    Вр
                                                                                                                                                                                                                                     Ş
                                                                                                                              망
                   δõ
                                                        В
                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madellein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561
                                                                                                                                                                                                                                                                            Matches 468; Conservative
                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 CATGTACCTGAACGAAGTCGCGGACAAGCATGGCCTGGGCCGTATTGACATCGTGGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203
                                                                                                                                                                                                                        427 gctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctgatggag 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 CCATGCTCATTTAGACATCGAGG 1
                                                                                                                                                 487 tacgcaaagcaacacgggattcccatccccggtcactcccaagaaccccgtggagcatggat 546
                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                  61
                                                                                                                                                                                                    1 gctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctgatggag 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cccggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcagctacga 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccgcttcattggaatgaagtcccgaggtatctacgaggccccagcaggcaccatccttta 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            catgtacctgaacgaagtcgcgggcaagcatggcgtgggccgtattgacatcgtggagaa 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTGTGAAGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coctgtgåaggtgaccaacgtcaaggatggcaccaccaccaccagacctccttggagctctt 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGACCCAGCCAAAGCCCCCAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggacccagccaaagcccccaacacccctgacattctcgagatcgagttcaaaaaaggggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCTACACGAAGACCCA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggctggaatcctggagaaccccaagaaccaagcgcctccaggtctctacacgaagaccca 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACCATCAGCTACGA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccatgctcatttagacatcgagg 895
cctccaggtctctacacgaagacccaggacccaggccaaagcccccaacacccctgacatt 666
                                                      gagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaaccaagcg 180
                                                                         gagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaaccaagcg 606
                                                                                                                            tacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagcatggat 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09998598
                                                                                                                                                                                                                                                                                  37.7%; Score 467.4; DB 7; Length 469; 99.8%; Pred. No. 1.9e-118; tive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                            0;
```

```
Qу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΩV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-933-524A-54674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-09-933-524A-54674
                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                        QУ
                                                                                                                                                                                                                                                                                          В
                                                                                                                            Ωy
                                                                                                                                                            Вþ
                                                                                                                                                                                         Qy
                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/528,409
PRIOR FILING DATE: 2000-05-17
PRIOR FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 116231
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 54674
LENGTH: 479
                                                             δÃ
                                                                                                 밁
                                  Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 54674, Application US/09933524A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 458; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/933,524A CURRENT FILING DATE: 2001-08-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From Various Libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Drmanac, Radoje T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 cctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccctgacatt 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 gtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggtatctac 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 acccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaagcatggc 360
                                                                                                                                                                                                                               140
                            183
                                                                                                                                                                                                                                                               123
                                                                                               260 actgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgcaa 319
                                                                                                              243 actgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgcaa
                                                                                                                                                            08
                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                      20 gtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatcct 79
                                                                                                                                                                                                                                                                                                                                                                         3 gtocagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatcct 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaaggatggcacc 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acceaccagacctccttdgagctcttcatgtacctgaacgaagtcgcggggcaagcatggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gagaccccagcaggcaccatcctttaccatgctcatttagacatcgagg 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggtatctac 846
                                                                                                                                                                             ggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttcat 199
                                                                                                                                                                                                                                           ggaagacttcgaggaagccaggaaggacggcactgaagcttggggccaaaaaggtgttcat 182
                                                                                                                                                                                                                                                                                         cgtgtggctgaaggaacaaggctatgacgtcgttgcctatctggccaacattggccagaa
                                                                                                                                                                                                                                                                                                        cgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccagaa 122
ggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaaggt 422
                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Labat, Ivan
Stache-Crain, Birgit
                                                                                                                                                                                                                                                                                                                                                                                                                                        36.9%; Score 457.4; DB 6; 99.8%; Pred. No. 1.1e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                            259
```

0,

QΥ

```
В
                                                                                                                                             Qy
                                                                                                                                                                                         밁
                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                              DЬ
                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-029-386-8869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-029-386-8869/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 8869
LENGTH: 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Penn, Sharron G.
APPLICANT: Mank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8869, Application US/10029386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: MAP TO AC005000.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.76

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4

OTHER INFORMATION: NUT HIT: 9114740527, EVALUE 0.00e+00

OTHER INFORMATION: SMISSPROT HIT: P00966, EVALUE 3.00e-74

OTHER INFORMATION: EST_HUMAN HIT: BE783168.1, EVALUE 0.00e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEO ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                   523 cccaagaacccgtggagcatggatgagaacctcatgcacatcagctacgaggctggaatc 582
                                                                                                            463 aagggccgcaatgacctgatggagtacgcaaagcaacacgggattcccatcccggtcact 522
                                                                                                                                                                                                                             404
                                                                                                                                                                                                                                                                                                        344
                                                                                                                                                                                                                                                                                                                                              284 ggccctgcatcgcccgcaaacaagtggaaatcgcccagcgggaggggggccaagtatgtgt 343
                                                                                                                                                                                                                                                                                                                                                                                                      418 TGGCCATCCAGTCCAGCGCACTGTATGAGGACCACTACCTCCTGGGCCACCTCTCTCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                           224 cggccatccagtccagcgcactgtatgaggaccgctacctcctggggcacctctctttgcca 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478 GGGGCAAAAAGGTGTTCATTGAGGAAGTCAGCAAGGAGTTTGTGAAGGAGTTCATCTGGC 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 gggccaaaaaggtgttcattgaggatgtcagcagggagtttgtgggggggttcatctggc 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 cattgctccctggaggatgcctgaattctacaaccggtt 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 cattgctccctggaggatgcctgaattctacaaccggtt 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380 ggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaaggt 439
            CCCAAGAACCTGTGGAACATGGACGAGAACCTCATGCAGATCAGCAATGAGGCTGGAATC
                                                                                       AAGGTCCGAAATGACCTTATGGAACACACAAAGCAACACGGGATTCCCATCCCAGTCACT 119
                                                                                                                                                                  TGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCCAAGTTCTACAACAGGTTC 179
                                                                                                                                                                                         tgg-cccccagataaaggtcattgctccctggaggatgcctgaattctacaaccggttc 462
                                                                                                                                                                                                                                                                    | CCCacggcgccacaggaaaggggaacgatcaggtccggtttgagctcagctgctactcac 403
                                                                                                                                                                                                                                                CCCACAGCGCCACAGGAAAGGGAAATGATCAGGTCCAGTTTGAGCTAAACTGCTACTCTC
                                                                                                                                                                                                                                                                                                                           TGGCCAACACTGGCCAGAAGGAAGACTTTGAGGAAGCCAGGAAGAAGGCACTGAAGCTTG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.6%;
91.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 454,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 9.7e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 8; Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>1</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                59
                                                                                                                                                                                                                                                                                                                               299
Search completed: February 12, 2002, 15:49:53 Job time: 9586 sec
```

```
В
                                                                                                                    Qy
                                                                                                                                                          B
                                                                                                                                                                                      γ
                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                               Ф
                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                            망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΩV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: n = A,T,C or US-09-922-340-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-922-340-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 266, Application US/09922340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR FILING DATE: 1998-01-07
NUMBER OF SEQ ID NOS: 12181
SOFTMARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/922,340 CURRENT FILING DATE: 2001-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-08-03 PRIOR APPLICATION NUMBER: 09/353,690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From cDNA Libraries Of Fetal Liver-Spleen and Infant Brain FILE REFERENCE: 20411-726CON2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hyseq,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                   754 atgtacctgaacgaagtcgcgggcaagcatggcgtgggc 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 465
                                                                361 cctgtgaaggtgaccaacgtcaaggatggtaccaccnaccagacctccttggagctcttc
                                                                                   634 gacccagccaaagcccccaacacccctgacattctcgagatcgagttcaaaaaaggggtc
                                                                                                                                     301 gacccagccaaagcccccaacacccctgacattctcgagatcgagttcaaaaaaggggtc 360
                                                                                                                                                                                                         241 gctggaatcctggagaaccccaagaaccaagcgcctccaggtctctacacgaagacccag
                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                 121 aaccggttcaagggccgcaatgacctgatggagtacgcaaagcaacatgggattcccatc 180
                                                                                                                                                                                                                                                                                                                                                                        454 aaccggttcaagggccgcaatgacctgatggagtacgcaaagcaacacgggattcccatc 513
                                                                                                                                                                                                                                                                                                                                                                                                                                            394 tgctactcactggccccccagataaaggtcattgctccctggaggatgcctgaattctac 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 aagtatgtgtcccacggcgccacaggaaaggggaacgatcaggtccggtttgaggtccagc
                                                                                                                                                                                                                                                                                                                                                                                                                         61 tgctactcactggccccccagataaaggtcattgctccctggaggatgcctgaattctac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 aagtatgtgtcccacggcgccacaggaaaggggaacgatcaggtccggtttgagctcagc 60
atgtacctgaacgaagtcgcgggcaagcatggcgtggcc 459
                                                                                                                                                                                                                              gctggaatcctggagaaccccaagaaccaagcgcctccaggtctctacacgaagacccag 633
                                                                                                                                                                                                                                                                                                   | coggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcagctacgag 573
                                                                                                                                                                                                                                                                              ccggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcagctacgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 453.2; DB 6; Length 465; Pred. No. 1.5e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
```

```
OM of: US-09-775-693-1 to: Pending_Patents_AA_Main:* out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                About: Results were produced by the GenCore software, version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: Feb 12, 2002 4:00 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database: Pending_Patents_AA_Main:*
Database sequences: 3148936
Database length: 277657034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query: US-09-//5-0
Query length: 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                search information block:
Query: US-09-775-693-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search time (sec): 324.520000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -MODEL-frame+_n2p.model -DEV=xlp
-Q-/cgn2_1/USPTO_spool/US09775693/runat_12022002_124153_1366/app_query.fasta_1.1315
-Q-/cgn2_1/USPTO_spool/US09775693/runat_12022002_124153_1366/app_query.fasta_1.1315
-Q-/cgn2_1/USPTO_spool/US09775693/runat_12022002_124153_1366/app_query.fasta_1.1315
-Q-/cgn2_1/USPTO_spool/US09775693/runat_1202200
-GAPEXT=0.000 -GAPEXT=4.000 -MINMATCH=0.100 -XGAPED=10.000
-XGAPEXT=0.000 -QGAPOD-4.500 -QGAPEXT=7.000 -YGAPOD=10.000
-XGAPEXT=0.500 -DELOP-6.000 -DELEXT=7.000 -YGAPOD=10.000
-YGAPEXT=0.500 -DELOP-6.000 -DELEXT=7.000 -YGAPOD=10.000
-YGAPEXT=0.500 -DELOP-6.000 -DELEXT=7.000 -YGAPOD=10.000
-YGAPEXT=0.500 -DELOP-6.000 -DELEXT=7.000 -YGAPOD=10.000
-YGAPEXT=0.500 -TANAS-human40.cdi -LIST=45 -DOCALIGN=200
-MATRIX-blosum62 -TRANS-human40.cdi -LIST=45 -DOCALIGN=200
-OUTFWT-pfs -NORM-ext -MINLEN=0 -MAXLEN=200000000
-OUTFWT-pfs -NORM-ext -MINLEN=0 -MAXLEN=200000000
-OUTFWT-S693_@CGN1_1_278 -NCDU=6 -ICPU=3 -LONGLOG -NO_XLPXY
/cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-177-646-3534 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyright (c) 1993-2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -THREADS=
```

```
/cgn2_6/ptodata/2/paa/US094_COMB.pep:US-09-401-151-18 + 895.00 1265.86 1.8e-62 /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-312-544-5456 + 894.50 1262.41 2.1e-62 /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-324-109-21424 + 894.50 1262.41 2.1e-62 /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-186-280-522 + 888.00 1261.26 5.4e-62 /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-195-311-672 + 881.50 1252.09 1.8e-61 /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-195-311-672 + 881.50 1252.09 1.8e-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/2/paa/US095_COMB.pep:US-09-538-092-835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
; Sequence 835, Application US/09538092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-538-092-835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           us^{2}-09-77\overline{5}-693-1 \times us-09-538-092-835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio: 5.204 Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-09-538-092-835 from: 1 to: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Polypeptide Accession Number P00966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: (0)...(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 ATCTGGCCAACATTGGCCAGAAGGAAGGCATTCGAAGAAGCCAGGAAGAAG
                                                                                                                                                                                                                                                                                 151 GCACTGAAGCTTGGGGCCAAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                             251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                            34 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                       67 uPheValGluGluPheIleTrpProAlaIleGlnSerSerAlaLeuTyrG
                                                                                                                                                                                                                                                                                                                               51 AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspValSerArgGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rSerCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT
                                                                                                                                       luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg 100
                                                                                          AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCCAAGTATGTGTCCCCACGG
                                                                                                                                                                                                                                                                                                                                                        Quality: 2144.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CuraPatSeqFormatter Version 0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34
                                                                                                                                                                                                                                                        84
```

```
1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
               1201 GAATATCATCGTCTCCAGAGGAAGGTCACTGCCAAA 1236
                                                                                                                               1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                       1051 GTGTCCGTCCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                              1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGGAAAGTGCAG 1050
401 GluTyrHisArgLeuGlnSerLysValThrAlaLys 412
                                                      367 uSerLeuTyrAsnGluGluLeuValSerMetAsnValGlnGlyAspTyrG 384
                                                                                                                                                                        351 ValSerValLeuLysGlyGlnValTyrIleLeuGlyArgGluSerProLe 367
                                                                                                                                                                                                                                334 alargHisCysTleAlaLysSerGlnGluArgValGluGlyLysValGln 350
                                                                                                                                                                                                                                                                                        317 eAlaGluLeuValTyrThrGlyLeuArgProSerProGluCysGluPheV 334
                                                                                                                                                                                                                                                                                                                                                951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                      801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   701 AGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 oAsnThrProAspIleLeuGluIleGluPheLysLysGlyValProValL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         651 CAACACCCCTGACATTCTCGAGATCGAGGTTCAAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 TyrAsnArgPheLysGlyArgAsnAspLeuMetGluTyrAlaLysGlnHi 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
```

```
seq_name: /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-775-693-7
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-693-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-775-693-7 from: 1 to: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-775-693-1 x US-09-775-693-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Clark, Mike
501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                          151 TyrasnargPheLysGlyArgAsnAspLeuMetGluTyrAlaLysGlnHi 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Holtsberg, Frederick Wayne
APPLICANT: Ensor, Charles Mark
TITLE OF INVENTION: Methods For Predicting Susceptibility Of Patients To Arginine
FILE REFERENCE: PHOE-0060
                                                                                              451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                  134 erLeuAlaProGlnIleLysValIleAlaProTrpArgMetProGluPhe 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/775,693
CURRENT FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                      401 CACTGGCCCCCCAGATAAAGGTCATTGCTGCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                              117 yAlaThrGlyLysGlyAsnAspGlnValArgPheGluLeuSerCysTyrS 134
                                                                                                                                                                                                                                                                  351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                      101 LysGlnValGluIleAlaGlnArgGluGlyAlaLysTyrValSerHisGl 117
                                                                                                                                                                                                                                                                                                                             301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCCAAGTATGTGTCCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                             151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTGATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspValSerArgGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 rSerCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetSerSerLysGlySerValValLeuAlaTyrSerGlyGlyLeuAspTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 2144.00
Ratio: 5.204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
```

/*

```
; Sequence 87, Application US/60239841
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLC
; FILE REFERENCE: PA-0038
; CURRENT APPLICATION UNMBER: US/60/239,841
; CURRENT FILING DATE: 2000-10-11
; NUMBER OF SEO ID NOS: 194
                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-239-841-87
                  SOFTWARE:
SEQ ID NO 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1001
                                                                                                                                                                                                                                                                                                                                                                                                 1201
LENGTH: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                               384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        551
                                                                                                                                                                                                                                                                                                                                                       401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plleValGluAsnArgPheIleGlyMetLysSerArgGlyIleTyrGluT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC
                                                                                                                                                                                                                                                                                                                                                                       GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrMetAspArgGluValArgLysIleLysGlnGlyLeuGlyLeuLysPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PheMetTyrLeuAsnGluValAlaGlyLysHisGlyValGlyArgIleAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCATGTACCTGAACGAAGTCGCGGGCCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnAlaProProGlyLeuTyrThrLysThrGlnAspProAlaLysAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValSerValLeuLysGlyGlnValTyrIleLeuGlyArgGluSerProLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alArgHisCysIleAlaLysSerGlnGluArgValGluGlyLysValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysValThrAsnValLysAspGlyThrThrHisGlnThrSerLeuGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oAsnThrProAspIleLeuGluIleGluPheLysLysGlyValProValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        snLeuMetHisIleSerTyrGluAlaGlyIleLeuGluAsnProLysAsn
                                                                                                                                                                                                                                                                                                                                                  GluTyrHisArgLeuGlnSerLysValThrAlaLys 412
                                                                                                                                                                                                                                                                                                                                                                                                                                            luProThrAspAlaThrGlyPheIleAsnIleAsnSerLeuArgLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \tt uSerLeuTyrAsnGluGluLeuValSerMetAsnValGlnGlyAspTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eAlaGluLeuValTyrThrGlyLeuArgProSerProGluCysGluPheV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERL
                                       Program
                                                                                                                                                   GENES EXPRESSED IN COLON
                                                                                                                                                     CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367
```

```
alignment_scores:
Quality: 2123.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1543330CD1
US-60-239-841-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-775-693-1 x US-60-239-841-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
              651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                              151
                                                                                                                                                                                                                                                                                                                                                                                 401 CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                   351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTTGAGCTCCAGCTGCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspValSerArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC
                                                                                                                                                                                                                                                                                          TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC
                                                                                                                                   ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC
                                                                                                                                                                                                                                           CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                 yAlaThrGlyLysGlyAsnAspGlnValArgPheGluLeuSerCysTyrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysGlnValGluIleAlaGlnArgGluGlyAlaLysTyrValSerHisGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uPheValGluGluPheIleTrpProAlaIleGlnSerSerAlaLeuTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA
oAsnThrProAspIleLeuGluIleGluPheLysLysGlyValProValL
                                                                  GlnAlaProProGlyLeuTyrThrLysThrGlnAspProAlaLysAlaPr
                                                                                                                                                                                                         sGlyIleProIleProValThrProLysAsnProTrpSerMetAspGluA
                                                                                                                                                                                                                                                                          TyrAsnArgPheLysGlyArgAsnAspLeuMetGluTyrAlaLysGlnHi
                                                                                                                                                                                                                                                                                                                                              erLeuAlaProGlnIleLysValIleAlaProTrpArgMetProGluPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-60-239-841-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.1.
99.515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   с
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412
                                                                                                                                                                                                         184
                                                                                                                                                                                                                                                                              167
                                                                                                                                                                                                                                                                                                                500
                                                                                                                                                                                                                                                                                                                                                                                  450
                                                                                                                                                                                                                                                                                                                                                                                                                                                     40C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
 234
                                                                    217
                                                                                                      650
                                                                                                                                       200
                                                                                                                                                                       600
                                                                                                                                                                                                                                           550
                                                                                                                                                                                                                                                                                                                                                  150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50
```

```
seq_documentation_block:
    Sequence 1594, Applicati
    GENERAL INFORMATION:
    APPLICANT: Craig Rosen,
    APPLICANT: Steve Ruben
    TITLE OF INVENTION: Hum
    FILE REFERENCE: PA101PC
    CURRENT APPLICATION NUM
    CURRENT EPPLICATION NUM
    CURRENT EPPLICATION NUM
    CURRENT FILING DATE: 20
    EARLIER APPLICATION NUM
    EARLIER FILING DATE: 19
    NUMBER OF SEO ID NOS. 1
                                                                                                                                                                                                                                                                  APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
ITILE OF INVENTION: Human Prostate Cancer Associated Gen
ITILE REFERENCE: PAIOIPCT
CURRENT APPLICATION NUMBER: PCT/US00/05988
CURRENT FILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: 60/124,270
EARLIER APPLICATION NUMBER: 60/124,270
EARLIER FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                           ; LOCATION: (22)
; OTHER INFORMATION:
PCT-US00-05988-1594
                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US00-05988-1594
                                                                                                                                                                                                                                         LENGTH: 442
TYPE: PRT
                                                                                                                                                                            NAME/KEY: SITE
                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                     ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 luProThrAspAlaThrGlyPheIleAsnIleAsnSerLeuArgLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alArgHisCysIleAlaLysSerGlnGluArgValGluGlyLysValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGGAAAGTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTGAGCTGGTGTATACCGGTTTACGGCCCTAGCCCTGAGTGTGAATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hrProAlaGlyThrTleLeuTyrHisAlaHisLeuAspTleGluAlaPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uSerLeuTyrAsnGluGluLeuValSerMetAsnValGlnGlyAspTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValSerValLeuLysGlyGlnValTyrIleLeuGlyArgGluSerProLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PheMetTyrLeuAsnGluValAlaGlyLysHisGlyValGlyArgIleAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ysValThrAsnValLysAspGlyThrThrHisGlnThrSerLeuGluLeu
  Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application PC/TUS0005988
                                                                                                                                                                                                                     sapiens
  2123.00
5.178
                                                                                                                             Xaa equals
                                                                                                                             any of
                                                                                                                             the naturally occurring
Length:
Gaps:
412
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences and Polypeptides
                                                                                                                             L-amino
                                                                                                                               acids
```

```
alignment_block:
US-09-775-693-1 x PCT-US00-05988-1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity: 99.515
   801
                                                                                                                    701
                                                                                                                                                 247
                                                                                                                                                                            651
                                                                                                                                                                                                         231
                                                                                                                                                                                                                                    601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC
                                                                                                                                                                                                                                                                  214
                                                                                                                                                                                                                                                                                                                          197
                                                                                                                                                                                                                                                                                                                                                      501
                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                            164
                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT
                                                                                                                                            CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA
                                                                                                                                                                                                                                                                                                                      CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA
CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA
                                                                                                                                                                                                       GlnAlaProProGlyLeuTyrThrLysThrGlnAspProAlaLysAlaPr
                                        TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheMetTyrLeuAsnGluValAlaGlyLysHisGlyValGlyArgIleAs
                                                                                    ysValThrAsnValLysAspGlyThrThrHisGlnThrSerLeuGluLeu
                                                                                                   AGGTGACCAACGTCAAGGATGGCACCACCACCAGCCTCCTTGGAGCTC
                                                                                                                                                                                                                                                               ACCTCATGCACCATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                 TyrAsnArgPheLysGlyArgAsnAspLeuMetGluTyrAlaLysGlnHi
                                                                                                                                                                                                                                                                                                                                                                                                                                          erLeuAlaProGlnIleLysValIleAlaProTrpArgMetProGluPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yAlaThrGlyLysGlyAsnAspGlnValArgPheGluLeuSerCysTyrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysGlnValGluIleAlaGlnArgGluGlyAlaLysTyrValSerHisGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uPheValGluGluPheIleTrpProAlaIleGlnSerSerAlaLeuTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspValSerArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: PCT-US00-05988-1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 99.272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442
                                                                                                                                                                                                                                                                                              600
                                                                                                                                                                                                                                                                                                                                                    . 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47
                              297
                                                                                      280
                                                                                                                                              264
                                                                                                                                                                           700
                                                                                                                                                                                                                                    650
                                                                                                                                                                                                                                                                                                                                                                                  197
                                                                                                                                                                                                                                                                                                                                                                                                               500
                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                         247
                                                                                                                                                                                                                                                                 230
                                                                                                                                                                                                                                                                                                                          214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150
```

97

```
seq_documentation_block;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US00-26524B-6180
                                                                                                                                                                                                                                     LOCATION: (22)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids PCT-US00-26524B-6180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Birse et. al.
APPLICANT: Birse et. al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
                                                                                                                                                                                   alignment_scores:
                                                                                                 alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6180, Application PC/TUS0026524B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297 pIleValGluAsnArgPheIleGlyMetLysSerArgGlyIleTyrGluT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        851 CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: PCT/US00/26524B
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/163,280
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 6180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1101
                                                 Align seg 1/1 to: PCT-US00-26524B-6180 from: 1 to: 442
                                                                                  US-09-775-693-1 x PCT-US00-26524B-6180
                                                                                                                                  Percent Similarity: 99.515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: PA005PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 8564 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                          ENGTH: 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uSerLeuTyrAsnGluGluLeuValSerMetAsnValGlnGlyAspTyrG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
                                                                                                                                                        Quality: 2123.00
Ratio: 5.178
                                                                                                                                               percent Identity: 99.272
```

```
101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 rSerCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 MetSerSerLysGlySerValValLeuAlaTyrSerGlyGlyLeuAspTh 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 ANACAAGTGGAAATCGCCCAGCGGGGGGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysTleAlaArg 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 AGGACCGCTACCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 AlaLeuLysLeudiyAlaLysLysValPheIleGluAspValSerArgGl 97
                                                                                                                                                                                                                                                                                                                                                                                                                            401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                  451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                        551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAAC 600
                                                                                                                                                                                                              601 CARGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGGCAAAGCCCC 650
                                                                                                                                                                    701 AGGTGACCAACGTCAAGGATGGCACCACCCAGCAGACCTCCTTGGAGCTC 750
                                                                                  281 PheMetTyrLeuAsnGluVaiAlaGlyLysHisGlyValGlyArglieAs 297
                                                                                                                                                751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                         314 hrProAlaGlyThrileLeuTyrHisAlaHisLeuAspIleGluAlaPhe 330
                                                               851 CCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                   901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      րրումանուննունունունունում արտարարու
```

```
alignment_block:
                                                                                                                                                                          Align seg 1/1 to: US-09-925-300-1594 from: 1 to: 442
                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                              US-09-925-300-1594
                                                                                                                                                                                                             us-09-77\bar{5}-693-1 \times us-09-925-300-1594
                                                                                                                                                                                                                                                   Quality: 2123.00 Length: 412
Ratio: 5.178 Gaps: 0
Percent Similarity: 99.515 Percent Identity: 99.272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/paa/US099_COMB.pep:US-09-925-300-1594
101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/925,300 CURRENT FILING DATE: 2001-08-10 PRIOR APPLICATION NUMBER: PCT/US00/05988 PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1594, Application US/09925300 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             FEATURE:

NAME/KEY: SITE
LOCATION: (22)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Craig Rosen, APPLICANT: Steve Ruben
                                             47 rSerCysileLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT 64
                                                             51 CTCGTGCATCCTCGTGTGGCCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                         LENGTH:
                                                                                                                                       1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 GluTyrHisArgLeuGlnSerLysValThrAlaLys 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414 luproThraspAlaThrGlyPheileAsnIleAsnSerLeuArgLeuLys 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 uSerLeuTyrAsnGluGluLeuValSerWetAsnValGlnGlyAspTyrG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442
```

```
1001 TCCGCCACTGCATCGCCAAGTCCCCAGGAGCGAGTGGGAAGGGGAAAGTGCAG 1050
347 eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 364
                                                                                    951 TGCTGAGCTGGTGTATACCGGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                              331 ThrMetAspArgGluValArgLysIleLysGinGlyLeuGlyLeuLysPh 347
                                                                                                                                             901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                             851 CCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                            801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                            297 pilevalGluAsnArgPheIleGlyMetLysSerArgGlyIleTyrGluT 314
                                                                                                                                                                                                                                                                                                                                            751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                             281 PheMetTyrieuAsnGluValAlaGlyLysHisGlyValGlyArglieAs 297
                                                                                                                                                                                                                                                                                                                                                                                            264 ysvalrhrasnvalLysaspGlyThrThrHisGinThrSerLeuGluLeu 280
                                                                                                                                                                                                                                                                                                                                                                                                                          701 AGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         651 CAACACGCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 oAsnThrProAspIleLeuGluIleGluPheLysLysGlyValProValL 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGGCCAAAGCCCC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 GlnAlaProProGlyLeuTyrThrLysThrGlnAspProAlaLysAlaPr 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 snLeuMetHisIleSerTyrGluAlaGlyIleLeuGluAsnProLysAsn 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 sGlylleProlleProvalThrProLysAsnProTrpSerMetAspGluA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TyrasnargPheLysGlyArgasnaspLeuMetGluTyralaLysGlnHi 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 erLeuAlaProGlnfleLysValfleAlaProfrpArgMetProGluPhe 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 CACTGGCCCCCCAGATAAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 yalaThrGlyLysGlyAsnAspGlnValArgPheGluLeuSerCysTyrS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 uPhevalGluGluPherieTrpProAlarieGinSerSerAlaLeuTyrG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys 80
```

```
seq_documentation_block:
; Sequence 2729, Application US/09760475
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ49
; CURRENT APPLICATION NUMBER: US/09/760,475
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4122
; NUMBER OF SEQ ID NOS: 4122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-760-475-2729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-760-475-2729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-09-760-475-2729 from: 1 to: 473
                                                                                                                                                                                                                                                                                                                                                                                                    US-09-775-693-1 x US-09-760-475-2729
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 2123.00
Ratio: 5.178
Percent Similarity: 99.515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2729
LENGTH: 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: SITE
LOCATION: (14)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                       95
                                                                                                                                                                                                                     78
                                                                                                                                                                                                                                    51 CTCGTGCATCCTCGTGTGGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rSerCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 99.272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                           95
```

1150 445	01 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG	11(
1100 428	51 GTGTCCGTCCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT	105
1050 411	01 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 	100 39
1000 395	51 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG	95 37
950 378	01 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 	90 36
900 361	51 CCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC	3 4 3 4
850 345	1 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 	80 32
800 328	1 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA	75 31
<u> </u>	1 AGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGGTC	70 29
700 295	1 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA	65 27
650 278	1 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAGCCCCC 	6 0
600 261	1. ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAAC	55 24
70 4	1 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA S	221
500 228	1 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 5	45: 21:
Ë 5	o — O	195
400 195	1 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 4	351 178
350 178	1 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCCACGG 3	301 162
300	1 AGGACCGCTACCTCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGC 3	251 145

401 CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
150 150
7
AGGACGGCTACCTCGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCC
201 GTTTGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAG
151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
Align seg 1/1 to: US-60-207-216-791 from: 1 to: 425
alignment_block: US-09-775-693-1 x US-60-207-216-791
alignment_scores: Quality: 1631.00 Length: 412 Ratio: 4.660 Gaps: 2 Percent Similarity: 84.951 Percent Identity: 80.825
: LENGTH: 425 ; LENGTH: 425 ; TYPE: PRT ; ORGANISM: HUMAN US-60-207-216-791
: NUMBER OF SEQ ID NOS: 898 : SOFTWARE: FastSEQ for Windows Version 4.0 : SEO ID NO 791
CURRENT APPLICATION NUMBER: US/60/207,216; CURRENT FILING DATE: 2000-05-26
; APPLICANT: Beasley, Ellen ; IITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS, ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS, ; TITLE OF INVENTION: AND USES THEREOF ; FILE REFERENCE: CL000580
<pre>seq_documentation_block: Sequence 791, Application US/60207216 GENERAL INFORMATION:</pre>
seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-207-216-791
1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGGTTGAAG 1200

-34811	seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08631
	1200 GGAATATCATCGTCTCCAGAGCAAGGTCACTGCC 1233
.199	1150 GAGCCAACTGATGCCACCGGGTTCAATAATCAATTCCCTCAGGCTGAA 1
L149 196	1100 TGTCTCTCTACAATGAGGAGCTGGTGAAGGTGAACGTGCAGGGTGATTAT 1
980	1050 GGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCAC 1
1049 363	1000 GTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCA 1
999 346	950 TTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTT (
949 330	900 CACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAAT ;
899 313	850 ACCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTT
849 296	800 ACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAG 280 spIleValGluasnCysPheIleGlyMetLysSerArgGlyIleTyrGlu
799 280	750 CTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTG
749 263	700 AAGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCT
699 246	650 CCAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTG
649 230	600 CCAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC
599 213	551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAA.CCCCAAGAA
550 197	501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA
500 180	451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA ::: 164 TyrAsnH1sPheLysGlyCysSerAspLeuThrGluTyrThrLysGlnHi
163	151GlnIleLysValIleAlaProTrpSerMetProGluPhe

seq_documentation_block:
 Sequence 34811, Application PC/TUS0108631
 GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc
 TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

```
alignment_block:
us-09-775-693-1 x PCT-US01-08631-34811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US01-08631-34811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: PCT-US01-08631-34811 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity: 86.916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 34811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: 09/540,217 PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 60736 SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/649,167 PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: PCT/US01/08631 CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: DOMAIN
LOCATION: (8)..(315)
OTHER INFORMATION: Arginosuccinate synthase domain identified by PFam, accession OTHER INFORMATION: name Arginosuc_synth, E-value=5.5e-151, PFam score of 481.4
NAME/KEY: misc_feature
LOCATION: (1)...(433)
OTHER INFORMATION: Xaa = X or * as defined in Table 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: DOMAIN
LOCATION: (112)..(157)
OTHER INFORMATION: Argininosuccinate synthase proteins domain identified by
OTHER INFORMATION: eMATRIX, accession number BL00564C, p-value=1.000e-40, raw score
OTHER INFORMATION: 25.47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 433
  401
                                            117
                                                                                       351
                                                                                                                                 101
                                                                                                                                                                          301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCCAAGTATGTCTCCCACGG 350
                                                                                                                                                                                                                                                            251
                                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG
                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE: 21272-049
                                                                                                                                                                                                                                      AGGACCGCTACCTCCTGGGCACCTCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC
                                        CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rSerCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT 34
                                                                                                                                                                                                                luAspArgTyrLeuLeuGlyThrPhePheAlaArgProCysIleAlaArg 100
                                                                                                                                                                                                                                                                                                                                                                                          AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspValSerArgGl 67
                                                                                                                             LysGlnValGluIleAlaGlnArgGluGlyAlaLysTyrValSerHisGl
                                                                                                                                                 Quality: 1603.50
Ratio: 4.310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 80.140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 433
                                                                                                                               117
  450
                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                               250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
```

	6 TCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236	120
1205 416	5 ACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATA :::: ::: ::: ProGlyPheIleGlnThrSerIleSerLeuLysAlaGluGlyAsnTy	116
116 4 400	1 TGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATGCC	112 38
1120 384	GTACATCCTCGGCCGGGA	1074 367
1073 367	CGAGTGGAAGGGAAAGTGCAG ArgValGluGlyLySSerAlaGly	1030 351
1029 350	3 GCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAG ::!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!	33 98 34 88
982 334	CCTGGGCTTGAAATTTGCTGAGCTGGTGTATACCGGTT	936 317
935 317	9 ATCGAGGCCTTCACCATGGACCGGGAAGTGCGCGAAAATCAAACAAGG 	30:
300	TCTACGAGACCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGAC	842 284
841 284	5 TATTGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTA ::: 7 TLeuThrSerTrpGluAsnArgPheHisTrpGluLeuLysSerArgGlyI	795 267
794 267	8 CTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCG 	748 251
747 250	1 AGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAG ::	701
700 234	1 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 	651 217
650 217	CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCCAAAGCCCCC	601 201
600 200	ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC	551 184
550 184	1 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGGATGGAT	501 167
500 167	TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA	451 151
150	$er Leu Ala Pro {\tt Gln IleLysValIleAlaProTrpArgMetPro {\tt GluPhe}$	134

seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08631-49199
seq_documentation_block:

Sequence 49199, Application PC/TUS0108631 GENERAL INFORMATION:
APPLICANT: Hyse, Inc APPLICANT: Hyse, Inc TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
AT APPLICATION NUMBER: PCT/UT APPLICATION NUMBER: PCT/UT TILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217 PRIOR FILING DATE: 2000-03-31 PRIOR APPLICATION NUMBER: 09/649,167
PRIOR NUMBEI SOFTWI
SEQ ID NO 49199 LENGTH: 385 TYPE: PRT
(N)
OTHER INFORMATION: Argininosuccinate synthase proteins domain identified by OTHER INFORMATION: eMATRIX, accession number BL00564A, p-value=1.231e-27, raw score OTHER INFORMATION: 19.93 NAME/KEY: DOMAIN
LOCATION: (8). (333) OTHER INFORMATION: Arginosuccinate synthase domain identified by PFam, accession OTHER INFORMATION: name Arginosuc_synth, E-value=7.7e-145, PFam score of 461.9 CT-US01-08631-49199
lignment_scores: Quality: 1431.50 Length: 407 Ratio: 4.618 Gaps: 2 Percent Similarity: 76.167 Percent Identity: 70.762
lignment_block: US-09-775-693-1 x PCT-US01-08631-49199
Align seg 1/1 to: PCT-US01-08631-49199 from: 1 to: 385
1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
51 CTCGTGCATCCTCGTGTGGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
101 ATCTGGCCAACATTGGCCAGAAGGAAGGACTTCGAGGAAGGCCAGGAAGAAG 150
151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
201 GTTTGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAG
251 AGGACCGCTACCTCGCGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGG 350 ::: ::: ::: 101 LysLysValGluThrValGlnArgValGlyAlaLysTyrGluGlyProTr 117
351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
17 pArg 1

1235	e: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-243-468-	seq_name
	1 GAATATCATCGTCTCCAGAGC 1221 GluTyrHisCysLeuGlnSer 334	120: 328
1200 327	1 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG	115: 31:
1150 311	1 GTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 	110: 29:
1100 294	1 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT	105: 278
1050 277	.CTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 	100: 26:
1000 261	gG	95; 241
247		24
950	1 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT	90:
247	7	24.
900	CCTTTACCATGCTCATTTAGA	85:
850 247	1 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 3 allevalGluAsn	80 24:
800 243	1 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 	75: 22:
750 226	1 AGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTC :: :::	70: 21:
700 210	1 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 	65 19
650 193	1 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGGCCAAAGCCCC	60: 17
600 176	1 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC	55: 16:
550 160	1 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAAGA	50: 14:
500 143	1 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA	45: 12:
126	9AlaproTrpArgMetproGluPhe	11

seq_documentation_block:
; Sequence 1235, Application US/60243468
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen

```
CURRENT APPLICATION NUMBER: US/60/243,468
CURRENT FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 2121
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1235
LENGTH: 317
TYPE: PRT
ORGANISM: HUMAN
US-60-243-468-1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-60-243-468-1235 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-775-693-1 x US-60-243-468-1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ISOLA TITLE OF INVENTION: NUCLE TITLE OF INVENTION: AND UP TITLE REFERENCE: CL000929
                                                                                                                                                                                      448
                                                                                                                                                                                                                            129
                                                                                                                                                                                                                                                                  398
                                                                                                                                                                                                                                                                                                        114
                                                                                                                                                                                                                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                                                                                                                                                       298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148
                                                                         162
               548 AGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAG 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ω
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 CACCTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGTTTGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGTCCAGCAAAGGCTCCGTG...GTTCTGGCCTACAGTGGCGGCCTGGA 47
                                                                                                                                                                                                                                                                                                                          CGGCGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCT 397
                                                                                                                                                                                                                                                                                                                                                                               AAGGCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAG 197
                                                                         nHisGlyIleProIleProValThrProLysAsnProTrpAsnMetAspG
                                                                                                             ACACGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATG 547
                                                                                                                                                                                                                                                                                                      gGlyAlaThrGlyGlu.....TyrGlnValArgPheGluLeuThrTrpT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gGluPheValGluGluPheIleTrpProAlaIleGlnSerSerThrLeuT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAG 147
                                                                                                                                                 TTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCA 497
                                                                                                                                                                                                                          yrSerLeuValProGlnIleLysGlyThrAlaProTrpArgMetProGlu 145
                                                                                                                                                                                                                                                                ACTCACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAA 447
                                                                                                                                                                                                                                                                                                                                                                                                                       CGCAAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laTyrLeuAlaAsnThrGlyGlnLysGluAspPheGluGluAlaArgLys
luAsnLeuMetHisIleSerTyrGluAlaGlyIleLeuGluAsnProLys 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 1390.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.680
86.842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOLATED HUMAN DRUG TARGET PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 4
Percent Identity: 81.287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50
                                                                             179
```

```
alignment_scores:
Quality: 1350.50
Ratio: 4.502
...-ilarity: 86.455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-212-664-486
                                                                                          alignment_block: us-09-775-693-1 \times us-60-212-664-486
                                                                                                                                                                                                                                                                     ; ORGANISM: HUMAN US-60-212-664-486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                          SEQ ID NO 486
LENGTH: 347
TYPE: PRT
                                                      Align seg 1/1 to: US-60-212-664-486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ladunga,
APPLICANT: Spier,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 486,
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HITTLE OF INVENTION: USES THEREOF FILE REFERENCE: CL000687
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 636 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/60/212,664
CURRENT FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      698 TGAAGGTGAACGTCAAGGATGGCACCCACCCAGCAGACCTCCTTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648 CCCCAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 AsnGlnValProProAsp.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 598 AACCAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  898 TTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 .....ArgValLysLysGlyValProV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             998 TTGTCCGCCACTGCATCGCCAAGTCC 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        948 ATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAAT 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 luThrProAlaGlyThrIleLeuTyrHisThrHisLeuAspIleLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             848 AGACCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 rAspIleValGluAsnArgPheThrGlyMetLysSerArgGlyTleTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       798 TGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 PhePheMetTyrLeuAsnGluValAlaAspLysHisGlyValGlyCysTh
1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt sPheAlaGluLeuValTyrThrAlaPheTrpHisSerProGluCysGluP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PheThrMetAspTrpGluValCysLysIleLysGlnGlyLeuGlyLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang, Yu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spier, Gene
Greenberg, Simon
Rabkin, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ladunga, Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/60212664
                                                                                                                                                       Percent Identity: 78.386
                                                            from: 1
                                                                                                                                                                                             Length:
                                                        to: 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN SECRETED PROTEINS, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
                          50
```

```
851 CCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                            801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGGAGGTATCTACGAGA 850
                                      901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                             204 ysValThrAsnValLysAspSerAlaThrHisGlnThrSerLeuGluLeu 220
                                                                                                                                                                                                                                                                                                                                                                                                                       187
                                                                                                                                                                                                                                                                                                                                                                                                                                                              651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleThrHis 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AlaLeuLysProGlyAlaLysLysMetLeuIleGluAspValAsnArgGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrMetTyrArgGluValHisLysIleLysGlnCysArgGlyLeuLysPh
                                                                                                                                                                                                                                              laProAlaGlyThrIleLeuCysTyrAlaHisLeuAspIleGluAlaPhe
                                                                                                                                                                                                                                                                                                                                                AGGTGACCAACGTCAAGGATGGCACCACCCACCCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                    CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                               oAsnThrProAspIleLeuGluIleGluPheLysLysGlyValProValL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnAlaProProAlaLeuTyrThrLysThrGlnAspProAlaLysThrPr 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gGlyIleProThrProValThrProLysAsnProTrpSerMetAspGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....GlyHisSerAspLeuThrGluTyrAlaLysGlnAr 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetSerSerLysGlySerIleValLeuAlaCysSerGlySerLeuAspTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: HUMAN US-60-216-770-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-216-770-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-60-216-770-97 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-775-693-1 x US-60-216-770-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity: 86.455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 97, Application US/60216770
GENERAL INFORMATION:
APPLICANT: Ladounga, Steven
APPLICANT: Spier, Eugene
APPLICANT: Greenberg, Simon
APPLICANT: Rabkin, Steven
APPLICANT: Wang, Yu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/60/216,770
CURRENT FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BONAZZÍ, VÍVÍCH
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 347
TYPE: PRT
101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                              151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                   67 uPheValGluGluPheIleTrpProAlaMetGlnSerSerThrLeuTyrG
                                                                                                                                                                                                                                                                                                                                       34 yrLeuAlaSerIleGlyGlnLysGluAspPheGlnGluAlaArgLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                     17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 ValAsnLeuSerAlaThrAlaSerProSerProArgSer 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
                                                                                    luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleThrHis 100
                                                                                                     AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCCCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                              rPheCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGC 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 1350.50
Ratio: 4.502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 78.386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                      84
                                                                                                                                                                                                                250
                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                                                                                                                                                            50
```

```
seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08631-49202
                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                             Sequence 49202, Application PC/TUS0108631
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 49202
                                                                CURRENT APPLICATION NUMBER: PCT/USO1/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 CGGGATTCCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                        304 ValAsnLeuSerAlaThrAlaSerProSerProArgSer 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                   992 GTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGC 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          951 TGCTGAGCTGGTGTATACCGGTTTAC......GGCCTAGCCCTGAGT 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 ThrMetTyrArgGluValHisLysIleLysGlnCysArgGlyLeuLysPh 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               snLeuMetHisIleSerCysGluAlaGlyIleLeuGluAsnProGluAsn 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnAlaProProAlaLeuTyrThrLysThrGlnAspProAlaLysThrPr 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aIleValGluAsnArgPheIleGlyThrLysSerArgGlyIleTyrArgA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eAlaGluLeuValTyrThrGly.PheTrpLeuSerGlyThrAlaLeuSer 303
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US01-08631-49202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: PCT-US01-08631-49202 from: 1 to: 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity: 80.449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-775-693-1 x PCT-US01-08631-49202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Arginosuccinate synthase domain identified by PFam, accession OTHER INFORMATION: name Arginosuc_synth, E-value=6.4e-68, PFam score of 217.6 NAME/KEY: misc_feature LOCATION: (1)...(487) OTHER INFORMATION: Xaa = X or * as defined in Table 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Argininosuccinate synthase proteins domain identified by OTHER INFORMATION: eMATRIX, accession number BL00564A, p-value=2.800e-37, raw sco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: DOMAIN
LOCATION: (24)..(272)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 19.93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: DOMAIN LOCATION: (23)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                            133 IValProThrGlyAlaThrGlyLysGlyAsnGluGlnValArgPheGluL 150
                                                                                                                                                                                                                                                                                                                                               117 AlaArgLysGlnValGlyAsnSerProSerGlyArgGlyAlaLysTyrVa 133
                                                                                                                                                                                                                                                                                                                                                                                                                                   100 yrGluAspArgTyrLeuProGlyHisLeuSerLeuProGlyProCysIle 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 ATGAGGACCGCTACCTCCTGGGC...ACCTCTCTTGCCAGGCCCTGCATC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:::||
183 rGlyLysAlaThrLeuGlyPheProIleProValThrProLysAsnProT
                                       489 CGCAAAGCAACAC...GGGATTCCCCATCCCGGTCACTCCCAAGAACCCGT 535
                                                                                        167
                                                                                                                                                                                                              389 TCAGCTGCTACTCACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGG 438
                                                                                                                                                                                                                                                                                                                                                                                         295 GCCCGCAAACAAGTG...GAAATCGCCCAGCGGGAGGGGGCCAAGTAT.. 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspValSerArgG1 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 rSerCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 uPheValGluGluPheIleTrpProAlaIleGlnValGlnAlaHisLeuT 100
                                                                                                                                                                         MetProGluPheTyrAsnArgPheLysGlyArgAsnAspLeuMetGluTy
                                                                                                                             ATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTA 488
                                                                                                                                                                                                                                                                                                        .GTGTCCCACGGCGCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGC 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 1314.00
Ratio: 3.670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..(60)
                                                                                                                                                                                                                                                                                      Percent Identity: 69.438
                  200
```

```
seq_documentation_block:
    Sequence 544, Application US/60185362
;    GENERAL INFORMATION:
    APPLICANT: Bonazzi, viven
    TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
    TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
;    TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-185-362-544
                                                                                                                                                                                                                                                                                                                     1205 ATCATCGTCTC...CAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                           1164 CACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG......GAAT 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1120 CTGGTGAGCATGAACGTG...CAGGGTGATTAT...GAGCCAACTGATGC 1163
                                                                                                                                                                                                                                                                                     447 yrHisArgLeuProArgAlaLysValThrCysGln 458
                                                                                                                                                                                                                                                                                                                                                                                             430 yHisArgGlySerSerLysHisGlnIleProPheLysAlaGluGlyAsnT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1079 TCCTC...GGCCGGGAGTCCCCA......CTGTCTCTCTACAATGAGGAG 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1003 CGCCACTGC.....ATCGCCAAGTCCCAGGAGCGAGTGGAAGG 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414 LeuValLysHisGlyThrCysLysGlyAspTyrTrpArgProlleAspGl 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397 leLeuSerGlyArgGluIleProHisCysLeuLeuThrMetArgGlu 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380 yLysGlyLysValGlnValValArgSerPheLysGlyProGlnValTyrI 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 ......CysProProThrGlyIleAlaLysValProArgLysProSerGl 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 luLeuValTyrThrGlyPheProAlaGlnAlaProGluCysGluPhe... 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 956 AGCTGGTGTATACCGGTTTA...CGGCCTAGCCCTGAGTGTGAATTTGTC 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 gGlySerCysGlyLysIleLysGlnGlyProGlyAlaTrpLysPheAlaG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          912 G...GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTG...AAATTTGCTG 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 SerPheTyrHisAlaHisLeuAspIleArgGlyLeuSerProTrpAspAr 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    865 ATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACC...ATGGACCG 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 lyAsn***SerProArgGlyIleLeuArgArgThrProAlaGlyHisHis 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               824 GAATGAAGTCC...CGAGGTATCTAC...GAGACCCCAGCAGGC...ACC 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 yLysHisGlyArgArgAlaValPheAspIleValGluAsnArgPheIleG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       777 CAAGCATGGCGTGGGCCGTATT...GACATCGTGGAGAACCGCTTCATTG 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 ThrHisGlnThrPheLeuGluLeuPheMetTyrLeuAsnGluValAlaGl 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     727 ACCCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGG 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 heLysLysGlyValProValGluGlyGlyProThrPheLysAspGlyThr 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          680 TCAAAAAAGGGGTCCCTGTGAAG...GTGACCAACGTCAAGGATGGCACC 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  636 CCCAGCCAAAGCCCCCAACACCCCT...GACATTCTC...GAGATCGAGT 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 586 GAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCTACACGAAGACCCCAGGA 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 rpSerMetAspGluAsnLeuMetHisIleSerTyrGluAlaGlyIleLeu 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    536 GGAGCATGGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTG 585
```

```
alignment_block:
US-09-775-693-1 x US-60-185-362-544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE: VARIANT
NAME/KEY: VARIANT
LOCATION: (1)...(299)
OTHER INFORMATION: Xaa = Any Amino
US-60-185-362-544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-60-185-362-544 from: 1 to: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity: 91.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: CL000285
CURRENT APPLICATION NUMBER: US/60/185,362
CURRENT FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 836
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 299
166 gPheIleGluMetLysSer***GlyIleCysLysThrProAlaGlyThrI 183
                                         866 TCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAA 915
                                                                                                                                       816 CTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCACCA 865
                                                                                                                                                                              150 GluValAlaGlyLysHisSerValGlyHisIleAspIleValGluAsnAr 166
                                                                                                                                                                                                                             766 GAAGTCGCGGGCAAGCATGGCCGTGGGCCGTATTGACATCGTGGAGAACCG 815
                                                                                                                                                                                                                                                                            716 AGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAAC 765
                                                                                                                                                                                                                                                                                                                                                                    117 ePheLysThrGlu...LysLysGlyValProValLysValThrSerIleL 133
                                                                                                                                                                                                                                                                                                                                                                                             666 TCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACGACCAACGTCA 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 LeuTyrMetLysIleGlnAspLeuAlaLysAlaProAsnThrProAsnIl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 616 CTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCTGACAT 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 GGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCA 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            566 GCTACGAGGCTGGAATCCTGGAGAACCCAAGAACCAAGCGCCTCCAGGT 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               466 GGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCATCCC 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        416 TAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 GAACGATCAGGTCCGGTTTGAGCTCAGCTGCTCACTGGCCCCCCAGA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 erHisGluAlaGlyIleLeuGluAsnProLysAsnGlnAlaProSerGly 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 GCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 oValThrLeuLysHisProTrpAsnMetAspGluAsnLeuMetHisIleS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GlyArgSerAspLeuMetGluTyrAlaGluLysHisGlyIleProIlePr 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 leLysValIleAlaProGlyArgIleProGluPheTyrAsnGlnSerLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 yAsnAspGlnValTrpPheGluLeuAlaCysTyrSerLeuAlaProGlnI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 1207.50
Ratio: 4.407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 77.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
```

916 200 966 216	GTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTA	965 216 1015 233
1016 233	CCAAGTCCCAGGAGCGAGTGGAAGGGGAAAGTGCAGGTGTCCTCAAG 1	1065 249
1066 250	GGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAATGA	1115 266
1116 266	GGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATGCCA 	1165 283
1166 283	CCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATATCATCGTCTC	1215 299

•			
•			
	•		
		·	
	·		
			•
	. .		

0.0034 0.0039 0.0048 0.0054 0.0053

```
Search information block:
Query: US-09-775-693-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Date: Feb 12, 2002 4:07 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database: Pending_Patents_AA_New:*
Database sequences: 216105
Database length: 44922408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM of: US-09-775-693-1 to: Pending_Patents_AA_New: * out_format : pts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query length: 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search time (sec): 443.280000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -MODEL-frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US99775693/runat_12022002_124153_1396/app_query.fasta_1.1315
-Q=/cgn2_1/USPTO_spool/US99775693/runat_12022002_124153_1396/app_query.fasta_1.1315
-DB=Pending_Patents_AA_new -OPWT=fastan -SUFFIX=rapn
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -QGAPOP=4.500 -CGAPEXT=0.500 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=bLOSUM62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THE_SCORE=PCt -THE_MAX=100 -THE_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=200000000
-USER=US09775693_@CGN1_1_44 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-981-353-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 87
LENGTH: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
```

```
/cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-53125 + /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-44261 + /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-70389 + /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-50632 + /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-77679 + 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-981-353-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-09-981-353-87 from: 1 to: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-775-693-1 x US-09-981-353-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 87, Application US/09981353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/981,353
CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lasek, Amy W. APPLICANT: Jones, David A. TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER FILE REFERENCE: PA-0038 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Incyte ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                              101 LysGlnValGluIleAlaGlnArgGluGlyAlaLysTyrValSerHisGl
                                                                                                                                                                                                                                                                                                                                                               301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 AGGACCGCTACCTCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 GCACTGAAGCTTGGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG
                                          401 CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 rSerCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                               84 luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspValSerArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetSerSerLysGlySerValValLeuAlaTyrSerGlyGlyLeuAspTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC
                                                                                                                                                                                                  CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 2123.00
: 5.178
: 99.515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 99.272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No: 1543330CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                               400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                  450
                                                                                                                                                                                                                                                                                                                                                                                350
                                                                                                                                                                                                                                                                                                                                                                                                                                                            100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136.50
135.50
134.00
133.00
132.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183.93
184.73
184.27
185.41
187.74
```

```
seq_documentation_block:
    Sequence 701, Application US/60340187
    GENERAL INFORMATION:
    APPLICANT: Tang, Y. Tom
    APPLICANT: Wang, Zhiwei
                                                                                                                                          seq_name: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:US-60-340-187-701
                                                                                                                                                                                                                                                                                                                                                                                                                                               1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1001
                                                                                                                                                                                                                                             1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      951 TGCTGAGCTGGTGTATACCGGTTTACGGCCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 PheMetTyrLeuAsnGluValAlaGlyLysHisGlyValGlyArgIleAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 GlnAlaProProGlyLeuTyrThrLysThrGlnAspProAlaLysAlaPr 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501 CGGGATTCCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 TyrAsnArgPheLysGlyArgAsnAspLeuMetGluTyrAlaLysGlnHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 erLeuAlaProGlnIleLysValIleAlaProTrpArgMetProGluPhe 150
                                                                                                                                                                                                                                                                                                                 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                             GluTyrHisArgLeuGlnSerLysValThrAlaLys 412
                                                                                                                                                                                                                                                                                     {\tt luProThrAspAlaThrGlyPheIleAsnIleAsnSerLeuArgLeuLys}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValSerValLeuLysGlyGlnValTyrIleLeuGlyArgGluSerProLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                     uSerLeuTyrAsnGluGluLeuValSerMetAsnValGlnGlyAspTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alArgHisCysIleAlaLysSerGlnGluArgValGluGlyLysValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrMetAspArgGluValArgLysIleLysGlnGlyLeuGlyLeuLysPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pIleValGluAsnArgPheIleGlyMetLysSerArgGlyIleTyrGluT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oAsnThrProAspIleLeuGluIleGluPheLysLysGlyValProValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sGlyIleProIleProValThrProLysAsnProTrpSerMetAspGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     snLeuMetHisIleSerTyrGluAlaGlyIleLeuGluAsnProLysAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167
```

```
alignment_block:
                                                                                                                                                                                        ; ORGANISM: Homo sapiens US-60-340-187-701
                                                                                                                           alignment_scores:
US-09-775-693-1 x US-60-340-187-701
                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1192
SOFTWARE: pt_FL_genes Version
SEQ ID NO 701
                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US01/14827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/491,404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                   LENGTH: 583
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/515,126 PRIOR FILING DATE: 2000-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/60/340,187
CURRENT FILING DATE: 2001-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Novel Nucleic Acids and TITLE OF INVENTION: Polypeptides FILE REFERENCE: 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/770,160
FILING DATE: 2001-01-26
APPLICATION NUMBER: PCT/US01/08656
FILING DATE: 2001-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-08-23
APPLICATION NUMBER: PCT/US01/08631
FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/04941
FILLING DATE: 2001-03-05
APPLICATION NUMBER: US 09/540,217
FILLING DATE: 2000-03-31
APPLICATION NUMBER: US 09/649,167
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/577,408 FILING DATE: 2000-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 09/552,929 FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/574,454
FILING DATE: 2000-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-02-26
APPLICATION NUMBER: US 09/519,705
FILING DATE: 2000-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 09/496,914
FILING DATE: 2000-02-03
APPLICATION NUMBER: US 09/560,875
FILING DATE: 2000-04-27
APPLICATION NUMBER: PCT/US01/03800
FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 09/577,409
FILING DATE: 2000-05-18
APPLICATION NUMBER: PCT/US01/04927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2000-01-25
APPLICATION NUMBER: PCT/US01/02623
FILING DATE: 2001-01-25
                                                                                                      Quality: 2036.00
                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boyle, Bryan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang, Jian-Rui
Ghosh, Malabik
                                                            5.168
99.244
                                                                                                                                                                                                                                                                                                                                                                            2000-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-04-18
                                                                                                                                                                                                                                                                                                                                     2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malabika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Radoje T
                                                            Percent Identity: 98.741
                                                                                                      Length:
```

Align seg 1/1 to: US-60-340-187-701

from: 1

to:

```
101 ATCTGGCCAACATTGGCCAGAAGGGAAGACTTCGAGGAAGCCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 uPheValGluGluPheIleTrpProAlaIleGlnSerSerAlaLeuTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 TyrAsnArgPheLysGlyArgAsnAspLeuMetGluTyrAlaLysGlnHi 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 erLeuAlaProGlnIleLysValIleAlaProTrpArgMetProGluPhe 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
                                                                                                                                                                                                                                                                                                                                                                                                                                                             277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 sGlyTleProIleProValThrProLysAsnProTrpSerMetAspGluA
                                                                                                                                                                                                                                                                                           310
                                                                                                                                                                                                                                                                                                                                                                         293 oAsnThrProAspIleLeuGluIleGluPheLysLysGlyValProValL 310
                                                                                                                                                               801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                   751
                                                                                                                                                                                                                                                                                                                                 701 AGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MetSerSerLysGlySerValValLeuAlaTyrSerGlyGlyLeuAspTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGACCGCTACCTCCTGGGCACCTCTCTTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                     CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                       ysValThrAsnValLysAspGlyThrThrHisGlnThrSerLeuGluLeu 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlnAlaProProGlyLeuTyrThrLysThrGlnAspProAlaLysAlaPr 293
ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                           CCCCAGCAGCACCATCCTTTACCATCCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                         pIleValGluAsnArgPheIleGlyMetLysSerArgGlyIleTyrGluT
                                                                                                                                                                                                           hrProAlaGlyThrIleLeuTyrHisAlaHisLeuAspIleGluAlaPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160
                                                  376
                                                                                                                                  360
```

```
seq_documentation_block:
; Sequence 1176, Applica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:US-60-340-187-1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Novel Nucleic Acids and TITLE OF INVENTION: Polypeptides FILE REPPORTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR APPLICATION NUMBER: PCT/US00/35017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tang, Y. Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/60/340,187
CURRENT FILING DATE: 2001-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                 PRIOR PRIOR
                                                                                                                                                                                                                                                                           PRIOR PRIOR PRIOR PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                                                               PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/491,404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                                                                                             PRIOR
PRIOR
PRIOR
                                                                                                                                                       PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTC 1191
                                                                                                                                                                                                                                                            PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 ThrMetAspargGluValArgLysTleLysGlnGLyLeuGlyLeuLysPh 393
                                      PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443 uSerLeuTyrAsnGluGluLeuValSerMetAsnValGlnGlyAspTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393 eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460 luProThrAspAlaThrGlyPheIleAsnIleLysPheLeu 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2001-02-26
APPLICATION NUMBER: US 09/519,705
FILING DATE: 2000-03-07
                                                                                                                                                                                                                                                                                       FILING DATE: 2001-02-05
APPLICATION NUMBER: US 09/515,126
FILING DATE: 2000-02-28
FILING DATE: 2000-02-28
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/03800 FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 09/560,875 FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/04927 FILING DATE: 2001-02-26
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 09/577,409
              FILING DATE: 2000-03-31
APPLICATION NUMBER: US 09/649,167
FILING DATE: 2000-08-23
                                                                            APPLICATION NUMBER:
                                                                                                                                    APPLICATION NUMBER: US 09/574,454 FILING DATE: 2000-05-19
                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                   APPLICATION NUMBER: PCT/US01/04941
APPLICATION NUMBER: PCT/US01/08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang, Zhiwei
Wang, Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ghosh, Malabika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weng, Gezhi
Boyle, Bryan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/60340187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-12-22
                                                                                                  2001-03-05
                                                                                                                                                                                                                                                                  2000-05-
                                                                                 US 09/540,217
```

```
alignment_block:
US-09-775-693-1 x US-60-340-187-1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(433)

OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set for US-60-340-187-1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-60-340-187-1176 from: 1 to: 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity: 86.916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: pt_FL_genes Version 6.0 SEQ ID NO 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US01/08656
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR EILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: PCT/US01/14827
PRIOR FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/770,160
PRIOR FILING DATE: 2001-01-26
                                          451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                      134 erLeuAlaProGlnIleLysValIleAlaProTrpArgMetProGluPhe 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 1192
                                                                                                                              401 CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                             117 yAlaThrGlyLysGlyAsnAspGlnValArgPheGluLeuSerCysTyrS
                                                                                                                                                                                                                     351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/552,929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                              301 AAACAAGTGGAAATCGCCCAGCGGGGGGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                251 AGGACCGCTACCTGCGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 ATCTGGCCAACATTGGCCAGAAGGAAGGAAGCTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                           84 luAspArgTyrLeuLeuGlyThrPhePheAlaArgProCysIleAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                               67 uPheValGluGluPheIleTrpProAlaIleGlnSerSerAlaLeuTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 rSerCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
TyrAsnArgPheLysGlyArgAsnAspLeuMetGluTyrAlaLysGlnHi 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 1603.50
Ratio: 4.310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 80.140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
```

```
1206 TCATCGTCTC...CAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                     1165 ACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG.......GAATA 1205
                                                                                                                                                                                                                                              1121 TGGTGAGCATGAACGTG...CAGGGTGATTATGAGCCAACTGAT...GCC 1164
                                                                                                                                                                                                                                                                                                                                                  1074 GTACATCCTCGGCCGGGAGTCCCCA...CTGTCTCTACAATGAGGAGC 1120
416 rHisArgLeuProArgAlaLysValThrAlaGln 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1030 CGAGTGGAAGGGAAA...GTGCAGGTGTCCGTCCTCAAGGGC...CAGGT 1073
                                                                                                 401 ProGlyPheIleGln...ThrSerIleSerLeuLySAlaGluGlyAsnTy 416
                                                                                                                                                                                                              384 euValLysHisGlyThrCysGlnGlyAspTyrGluProAsn***LeuPro 400
                                                                                                                                                                                                                                                                                                                      367 sThrSerLeuGlyProGluValProHisCysSerLeuTyrAsnGluGluL 384
                                                                                                                                                                                                                                                                                                                                                                                                                                351 ArgValGluGlyLysSerAlaGlyValProSerLeuLysGlyProArgCy 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 laProGluCysGluLeuValGlyProCysLeuArgGlnSerProGlnGlu 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           983 GCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCC...CAGGAG 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 yLeuGlyPheGluPheValGluLeuGlyValTyrArgPheSerGlyThrA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                842 TCTACGAGACCCCA...GCAGGCACCATCCTTTACCATGCTCATTTAGAC 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     936 CCTGGGCTTGAAATTTGCTGAGCTG...GTGTATACCGGGTTTACGGCCTA 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 IleGluAlaPheThrMetGlyGlyAspArgAlaGlnIleProAsnGlnGl 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             889 ATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAATC...AAACAAGG 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 rLeuThrSerTrpGluAsnArgPheHisTrpGluLeuLysSerArgGlyI 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              795 TATTGACATCGTGGAGAACCGCTTC...ATTGGAATGAAGTCCCGAGGTA 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 LeuPheMetTyrLeuAsnGluValAlaGlyLysHisGlyValGlyProTy 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         748 CTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGC...CG 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               701 AG...GTGACCAACGTCAAGGATGGCACCCACCAGCACCTCCTTGGAG 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 GlnAlaProProGlyLeuTyrThrLysThrGlnAspProAlaLysAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 snLeuMetHisIleSerTyrGluAlaGlyIleLeuGluAsnProLysAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC 600
```

seq_documentation_block:

Sequence 9692, Appli GENERAL INFORMATION:

Application US/10015127

APPLICANT: Bower, Stanley G. APPLICANT: Hinkle, Gregory J. APPLICANT: Slater, Steven C.

seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-015-127-9692

```
; TYPE: PRT ; ORGANISM: Sphingomonas elodea US-10-015-127-9692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
us-09-775-693-1 x us-10-015-127-9692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio: 3.065
Percent Similarity: 75.490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-10-015-127-9692 from: 1 to: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/252,455
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 14357
SEQ ID NO 9992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/015,127
CURRENT FILING DATE: 2001-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof FILE REFERENCE: 38-10(15806)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 AGGAAGAAGCCACTGAAGCTTGGGGCCCAAA.....AAGGTGTTCATTGA 185
                                                                                                                                                                                                                                                                                                                                                                                        386 AGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                    116 palaValSerHisGlyAlaThrGlyLysGlyAsnAspGlnValArgPheG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 GTATGTGTCCCACGGCGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 CCCTGCATCGCCCGCAAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 CCAGCGCACTGTATGAGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 TCATTGCCTATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 pThrSerValIleLeuLysTrpLeu...GlnGlnThrTyrAsnCysGluV 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 CACCTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTAT.....GACG 91
                                                                                                                                                                                            486 GTACGCAAAGCAACACGGGATTCCCATCCCGGTCACTCCCAAG.....A 529
                                                                                                                                                                                                                                                                                         436 AGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGA 485
                                                                                                                                                                                                                                                                                                                                       66 uAspValArgGluGluPheValLysAspTyrValPheProMetMetArgA 83
                                                                                                                                             162 uPheAlaGluSerHisGlnIleProValThrLysAspLysArgGlyGluS 179
                                                                                                                                                                                                                                          150 ArgGluTrpAspLeuThrSerArgThrLys.....LeuIleGl 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 ATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCTACACGAAGAC 629
                                                                                               530 ACCCGTGGAGCATGGATGAGAACCTCATGCACCATCAGCTACGAGGCTGGA 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetSerAspLysIleAsnArgValValLeuAlaTyrSerGlyGlyLeuAs 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGTCCAGCAAA...GGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgLysLysAlaGluMetAlaGlyValLysProGluHisIlePheIleGl 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProLeuIleAlaLysArgGlnIleGluIleAlaLysLeuValGlyAlaAs 116
                                                   ::|||:::||| ||| |||||||:::||| ||| |||:::
erProPheSerThrAspAlaAsnLeuLeuH1sThrSerSerGluG1yLys 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  944.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 48.529
```

```
seq_documentation_block:
    Sequence 79358, Application US/09708427
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-79358
                                                                                                                                                                                   FILE REFERENCE 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin Version 3.1
SEQ ID NO 79358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                630 CCAGGACCCAGCCAAAGCCCCCAACACCCCTGACATTCTCGAGATCGAGT 679
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1080 CCTCGGCCGGGAGTCCCCACTGTCTCTACAATGAGGAGCTGGTGAGCA 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1030 CGAGTGGAAGGGAAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTACAT 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  730 CACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 680 TCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATGGCACCACC 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 rValAsnProGluAspAlaProAspMetProGluThrIleThrIleAspP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1130 TG...AACGTGCAGGGTGATTATGAGCCAACTGATGCCACCGGGTTCATC 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       830 AGTCCCGAGGTATCTACGAGACCCCAGCAGGCACCATCCTTTACCATGCT 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 sHisGlyIleGlyArgLeuAspLeuValGluAsnArgPheValGlyMetL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   780 GCATGGCGTGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGA 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 AlaMetSerProAlaThrLeuLeuThrAlaLeuAsnGluLeuGlyArgLy 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1177 AACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           930 ACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTACGGC 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        880 CATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAATCAA 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 heSerProGluArgGluMetLeuGlnAlaAlaValAspTyrSerGlnGlu 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 HisArgGlyIleGluGlnIleThrLeuAspArgGlyAlaAlaHisLeuLy 307
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1.425
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
                                                                                                                        TYPE: PRT ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 lThrGlyArgLysSerProTyrSerLeuTyrSerGluLysValValThrP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 LysvalThrGlyThrValArgLeuLysLeuTyrLysGlyScrValIleVa 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            980 CTAGCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAG 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391 LysLeuAsnAlaLeuArgLeuArg 398
                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heGluArgGlyAspGlyValAlaLeuAsnGly......Gln 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sAspGluLeuAlaProArgTyrAlaGluLeuIleTyrAsnGlyPheTrpP 324
                                                                                                                                                                           425
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 1..425
; OTHER INFORMATION: Ceres Seq. ID 1965189
US-09-708-427-79358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-09-708-427-79358 from: 1 to: 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 866.50
Ratio: 2.947
Percent Similarity: 74.809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-775-693-1 x US-09-708-427-79358
242 uTyrLeuGluIleGlyIleIleAlaGlyValProValSerIle...AsnG 258
                                                                                                          663 CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                                                                                                                    226 AspMetTyrMetMetSerIleAlaProGluAsnAlaProSerLysProGl 242
                                                                                                                                                                                              613 GGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCTGA 662
                                                                                                                                                                                                                                                                                                                            192 1ProvalSerLysLysSerIleTyrSerArgAspArgAsnLeuTrpHisL 209
                                                                                                                                                                                                                                      209 euSerHisGluGlyAspIleLeuGluAspProAlaAsnGluProLysGlu 225
                                                                                                                                                                                                                                                               513 CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                                                                                                                               463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGGATTCCCAT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 AGATAAAGGTCATTGCTCCCTGGAGGATGCCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 sGlyAsnAspGlnValArgPheGluLeuThrPheTyrAlaLeuAsnProG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 ValalaLysGluValGlyAlaAspAlaValAlaHisGlyCysThrGlyLy 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 ATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 euLeuGlyThrSerMetAlaArgProValIleAlaLysAlaMetValAsp 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 TCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 uTyrIleTyrProCysLeuArgAlaGlyAlaValTyrGluArgLysTyrL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 GCCAGAAGGAA...GACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 GlyAlaCysGlnLeuValValLysAspLeuLysGluGluPheValSerG1 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 lyGlnGlyAlaIleGluLeuGluGlyLeuGluLysLysAlaLysAlaSer 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 pLeuArgGluAsnTyrGlyCysGluValValCysPheThrAlaAspValG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 ValValLeuAlaTyrSerGlyGlyLeuAspThrSerValIleValProTr 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 45.547
```

```
alignment_block:
US-09-775-693-1 x US-09-708-427-79357
                                                                                                                                    alignment_scores:
                                                                                                                                                                                                     ; NAME/KEY: misc_feature 15 dry minio dCld; CorTiON: 1.446; COTHER INFORMATION: Ceres Seq. ID 1965188 US-09-708-427-79357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
   Sequence 79357, Application US/09708427
   GENERAL INFORMATION:
   APPLICANT: N. ALEXANDROV et al.
                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-79357
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
SEQ ID NO 79357
LENGTH: 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1..446
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1163 CCACCGGGTTCATCAACATCAATTCCCTC 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1113 TGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1063 AAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404 laGluGlyPheIleArgLeuTyrGlyLeu 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387 gGluAspIleSerSerPheGluAsnGlyGluIleTyrAsnGlnAlaAspA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 LysGlySerValAsnValAlaSerArgLysSerProTyrSerLeuTyrAr 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 etGluLysValThrAlaThrThrThrGlySerValThrLeuLysLeuTyr 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 lTyralaGlyArgTrpPheAspProLeuArgGlnSerPheAspAlaPheM 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         963 GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     913 GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 hrIleMetAlaAlaAlaValArgGluLeuGluSerLeuThrLeuAspArg 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      813 CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 nArgLeuValCysMetLysSerArgGlyValTyrGluThrProGlyGlyT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          763 AACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAA 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 lyArgAsp.....LeuSerProAlaSerLeuLeuAlaGluLeu 270
                                                                                                               Quality:
                                                                                            Ratio:
                                                                   866.50
2.947
74.809
                                                            Percent Identity: 45.547
                                                                                                        Length:
```

4

```
Align seg 1/1
       325
                                               863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG
                                                                                                                                                                                                                                                                                       279 lyArgAsp......LeuSerProAlaSerLeuLeuAlaGluLeu
                                                                                                                                                                                                                                                                                                                                    713 TCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATGTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         563 TCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 ValAlaLysGluValGlyAlaAspAlaValAlaHisGlyCysThrGlyLy 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 ATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 uTyrileTyrProCysLeuArgAlaGlyAlaValTyrGluArgLysTyrL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 GTTCATCTGGCCGGCCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 GlyAlaCysGlnLeuValValLysAspLeuLysGluGluPheValSerGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 GTGGTTCTGGCCTACAGTGGCCGGCCTGGACACCTCGTGCATCCTCGTGTG
nArgLeuValCysMetLysSerArgGlyValTyrGluThrProGlyGlyT
                                                                                                                                              CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCA 862
                                                                                                                                                                                                                                          AACGAAGTCGCGGCCAAGCATGGCGTGGGCCCGTATTGACATCGTGGAGAA 812
                                                                                                                                                                                                                                                                                                                                                                                      uTyrLeuGluIleGlyIleIleAlaGlyValProValSerIle...AsnG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                   CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspMetTyrMetMetSerIleAlaProGluAsnAlaProSerLysProGl 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lProValSerLysLysSerIleTyrSerArgAspArgAsnLeuTrpHisL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt ThrGlyArgGluAspAlaIleGluTyrAlaLysLysHisAsnValProVa}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCAT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              euLeuGlyThrSerMetAlaArgProValIleAlaLysAlaMetValAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lyGlnGlyAlaIleGluLeuGluGlyLeuGluLysLysAlaLysAlaSer 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValValLeuAlaTyrSerGlyGlyLeuAspThrSerValIleValProTr 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sGlyAsnAspGlnValArgPheGluLeuThrPheTyrAlaLeuAsnProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCAGAAGGAA...GACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pLeuArgGluAsnTyrGlyCysGluValValCysPheThrAlaAspValG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: US-09-708-427-79357 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196
                                                 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
```

```
alignment_block:
US-09-775-693-1 x US-09-708-427-55743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; LOCATION: 1..426
; OTHER INFORMATION: Ceres
US-09-708-427-55743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
    Sequence 55743, Application US/09708427
    GENERAL INFORMATION:
    APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-55743
                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-09-708-427-55743 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: Patentin version 3.1 SEQ ID NO 55743 LENGTH: 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 1..426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1163 CCACCGGGTTCATCAACATCAATTCCCCTC 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1113 TGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1063 AAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 GCCAGAAGGAA...GACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 laGluGlyPheIleArgLeuTyrGlyLeu 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408 gGluAspIleSerSerPheGluAsnGlyGluIleTyrAsnGlnAlaAspA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 etGluLysValThrAlaThrThrGlySerValThrLeuLysLeuTyr 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392 LysGlySerValAsnValAlaSerArgLysSerProTyrSerLeuTyrAr 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 lTyrAlaGlyArgTrpPheAspProLeuArgGlnSerPheAspAlaPheM 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           913 GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   963 GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012
                                                                                                           46 pLeuArgGluAsnTyrGlyCysGluValValCysPheThrAlaAspValG
                                                                                                                                                                                                                   30 Val***LeuAlaTyrSerGlyGlyLeuAspThrSerVallleValProTr 46
                                                                                                                                                                                                                                                                         19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG
GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                845.50
2.936
74.036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.501
                                                                                                                                                                                                                                                                                                                              to: 426
                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358
```

```
663 CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    613 GGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCCTGA 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         563 TCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 lProValSerLysLysSerIleTyrSerArgAspArgAsnLeuTrpHisL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          513 CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 ThrGlyArgGluAspAlaIleGluTyrAlaLysLysHisAsnValProVa 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCAT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413 AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 ValAlaLysGluValGlyAlaAspAlaValAlaHisGlyCysThrGlyLy 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 ATCGCCCAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       763 AACGAAGTCGCGGCCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAA 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 lyArgAsp.....LeuSerProAlaSerLeuLeuAlaGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 TCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 uTyrIleTyrProCysLeuArgAlaGlyAlaValTyrGluArgLysTyrL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 GlyAlaCysGlnLeuValValLysAspLeuLysGluGluPheValSerGl 96
etGluLysValThrAlaThrThrGlySerValThrLeuLysLeuTyr 370
                                                                                                                                                                                                                 GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012
                                                                                                                                                                                                                                                                                         GluThrMetGlnTrpLysAspIleIleAlaLeuLysTyrAlaGluLeuVa
                                                                                                                                                                                                                                                                                                                           GAAGTGCGCAAAATCAAACGCCTGGGCTTGAAATTTGCTGAGCTGGT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                  hrIleMetAlaAlaValArgGluLeuGluSerLeuThrLeuAspArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nArgLeuVal***MetLysSerArgGlyValTyrGluThrProGlyGlyT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGCA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnGluIleGlyGlyLysHisGlyIleGlyArgIleAspMetValGluAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATGTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uTyrLeuGluIleGlyIleIleAlaGlyValProValSerIle...AsnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspMetTyrMetMetSerIleAlaProGluAsnAlaProSerLysProGl 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 euSerHisGluGlyAspIleLeuGluAspProAlaAsnGluProLysGlu 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                            lTyrAlaGlyArgTrpPheAspProLeuArgGlnSerPheAspAlaPheM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258
```

```
alignment_block: us-09-708-427-55742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-708-427-55742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 55742, Application US/09708427
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-55742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-09-708-427-55742 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOPTWARE: PatentIn version 3.1
SEQ ID NO 55742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: N. ALEXANDROV et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1..447
OTHER INFORMATION: Ceres Seq. ID 1935961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Zea mays subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1063 AAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTACAA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..447
OTHER INFORMATION: Xaa is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1163 CCACCGGGTTCATCA 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1113 TGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                 101 GlyAlaCysGlnLeuValValLysAspLeuLysGluGluPheValSerGl 117
                                                                                                                                                                                                                                                       163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 ProArgGlySerSer 408
                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                69 GCTGAAGGAACAA...GGCTATGACGTCATTTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 Val***LeuAlaTyrSerGlyGlyLeuAspThrSerValIleValProTr 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gGluAspIleSerSerPheGluAsnGlyGluIleTyr.AsnGln***Thr 403
euLeuGlyThrSerMetAlaArgProValIleAlaLysAlaMetValAsp
                  TCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                  GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC
                                                                                                                                                                                                                                                    GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                      lyGlnGlyAlaIleGluLeuGluGlyLeuGluLysLysAlaLysAlaSer 100
                                                                                                                                                                                                                                                                                                                                                      GCCAGAAGGAA...GACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                         pLeuArgGluAsnTyrGlyCysGluValValCysPheThrAlaAspValG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt LysGlySerValAsnValAlaSerArgLysSerProTyrSerLeuTyrAr}
                                                                                                  uTyrIleTyrProCysLeuArgAlaGlyAlaValTyrGluArgLysTyrL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       845.50
2.936
74.036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 447
  150
                                                                                                                                                    262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387
                                                                                                    134
                                                                                                                                                                                                                                                                                                                                                                                                              84
```

```
1063 AAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCCACTGTCTCTCTACAA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                            184 luLeuLysValValAlaProTrpArgGluTrpAsp......Ile 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 ValAlaLysGluValGlyAlaAspAlaValAlaHisGlyCysThrGlyLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 ThrGlyArgGluAspAlaIleGluTyrAlaLysLysHisAsnValProVa 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                          1113 TGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 uTyrLeuGluIleGlyIleIleAlaGlyValProValSerIle...AsnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 AspMetTyrMetMetSerIleAlaProGluAsnAlaProSerLysProGl 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       613 GGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCCTGA 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563 TCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             513 CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                           1163 CCACCGGGTTCATCA 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        813 CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAGCAGGCA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 lyArgAsp.....LeuSerProAlaSerLeuLeuAlaGluLeu 291
                                                                                                                                                                                                                                                                                                                                                                             375 etGluLysValThrAlaThrThrGlySerValThrLeuLysLeuTyr 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 lTyrAlaGlyArgTrpPheAspProLeuArgGlnSerPheAspAlaPheM 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       963 GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 GluThrMetGlnTrpLysAspIleIleAlaLeuLysTyrAlaGluLeuVa 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  913 GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 hrIleMetAlaAlaAlaValArgGluLeuGluSerLeuThrLeuAspArg 341
425 ProArgGlySerSer 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATGTACCTG 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lProValSerLysLysSerIleTyrSerArgAspArgAsnLeuTrpHisL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCCAT 512
                                                                                                                                                                                                                                                  LysGlySerValAsnValAlaSerArgLysSerProTyrSerLeuTyrAr 408
                                                                                                                          gGluAspIleSerSerPheGluAsnGlyGluIleTyr.AsnGln***Thr 424
                                                                                                                                                                                                                                                                                          :::=:::===
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167
```

```
seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-897-516-5764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 ATCGCCCAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Xenorhabdus sp
US-09-897-516-5764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-09-897-516-5764 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-775-693-1 x US-09-897-516-5764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 5764
LENGTH: 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5764, Application US/09897516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Krasomil-Osterfeld, Karina C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Corbin, David R. APPLICANT: Goldman, Barry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-66-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 8409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Xenorhabdus sp. Genome FILE REFERENCE: 38-21(51847)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Slater, Steven C. APPLICANT: Spiridonov, Sergei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                             410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                           131 yLysGlyAsnAspGlnValArgPheGluSerThrTyrThrAlaLeuAlaP
                                                                                                                                                                                           360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                            115 GluLeuAlaLeuLysValGlyAlaAspAlaLeuAlaHisGlyAlaThrGl 131
                                                                                                                                                                                                                                                                                         310 GAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                       260 ACCTCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 TTGGCCAG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                     65 SerGlyAlaSerGluCysHisIleAlaAspLeuArgGluGluPheIleLy 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 pLeuLysGluHisTyrGlyAsnCysAspValIleAlaPheValAlaAspV 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 GCTGAAGGAACAA.....GGCTATGACGTCATTGCCTATCTGGCCAACA 112
                                                                                                                                                                                                                                                                                                                                               98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 alGlyGlnSerArgGluAspLeuGluGlyIleGluGlnLysAlaLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 IleValLeuAlaTyrSerGlyGlyLeuAspThrSerAlaIleIleProTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG
                                                  yrLeuLeuGlyThrSerMetAlaArgProIleIleAlaLysAlaGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malvar, Thomas M. Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     819.50
2.836
71.358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.185
                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                                                      114
                                                            160
```

```
Seq_documentation_block:

Sequence 11258, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-11258
CURRENT APPLICATION NUMBER: US/09/708,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1110 CAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTG 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1060 CTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTA 1109
                                                                                                                                                                                                                                                                                                                                                                                                            1210 CGTCTCCAGAGCAAG 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1010 GCATCGCCAAGTCCCAGGAGCGAAGGGAAAAGTGCAGGTGTCCGTC 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356 TyrLysGlyGlnValThrAlaThrGlnLysThrSerProHisSerLeuTy 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 laAlaGluMetLeuAlaGluAsnValSerGlyGluValIleLeuLysLeu 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 lValTyrAspGlyArgTrpPheValProLeuArgGlnSerIleGlnAlaA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   960 GGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACT 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 810 GAACCGCTTCATTGGAATGAAGTCCCGAGGGTATCTACGAGACCCCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 snGlyLysIleLeuSerProTyrGlnCysLeuAsnGlu...... 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      660 TGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 LysAspCysTrpGluTrpThrValGluProGluAspAlaProAspGluPr 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               610 CCAGGTCTCTACACGAAGACCCAGGGACCCAAGCCCAAAAGCCCCCAACACCCC 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          560 ACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 oThrThrAlaThrLeuGluLysIleTyrSerArgAspGluAsnAlaTrpH 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              510 CATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 LeuArgSerArgGluAlaLeuLeuAspTyrLeuLysValArgAspIlePr 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isAlaGluGlyPheIleArgLeuHisSerLeuSer...SerArgIleArg 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATATCAT 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rSerGluGluPheAlaThrPheGlyGluAspGluValTyrAspHisSerH 389
                                                                                                                                                                                                                                                                                                                                                 AlaLeuLysSerLys 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lyThrIleMetMetAlaAlaLeuArgGlyIleGluGlnLeuValLeuAsp 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oGluTyrLeuSerValThrValGluLysGlyGluValValGlyVal...A 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCT 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGAC 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uAsnArgLeuValGlyMetLysSerArgGlyCysTyrGluThrProGlyG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTCATGTAC 759
```

```
; NAME/KEY: misc_feature
; COATION: 1..498
; OTHER INFORMATION: Ceres Seq. ID 1822815
US-09-708-427-11258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-775-693-1 x US-09-708-427-11258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-09-708-427-11258 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1..498
OTHER INFORMATION: Xaa is any amino acid
                                                                 265 lProValThrLysLysSerIleTyrSerArgAspArgAsnLeuTrpHisL 282
                                                                                                                                                                                                                                                                 236 luLeuLysValValAlaProTrpArgGluTrpGlu......Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Arabidopsis thaliana FEATURE:
                       563 TCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCA 612
                                                                                                                      513 CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                     249 GlnGlyArgGluAspAlaIleGluTyrAlaLysLysHisAsnValProVa 265
                                                                                                                                                                                                                          463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCAT 512
                                                                                                                                                                                                                                                                                                                                   413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 ATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|||||| :::||| ::::|| :::::::|||| :::|||| :::||||| :::||||| 194 pPheIlePheProCysLeuArgAlaGlyAlaIleTyrGluArgLysTyrL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 TCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 GlyAlaSerGlnLeuValValLysAspLeuThrGluGluPheValLysAs 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 lyGlnGlyIleLysGluLeuGluGlyLeuGluGlnLysAlaLysAlaSer 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 GCCAGAAG...GAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 pLeuLysGluAsnTyrGlyCysGluValValCysPheThrAlaAspValG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 ValValLeuAlaTyrSerGlyGlyLeuAspThrSerVallleValProTr 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 GTGGTTCTGGCCTACAGTGGCGGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                        AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                             ......ValArgPheGluLeuThrPhePheSerLeuAsnProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            euLeuGlyThrSerMetAlaArgProValIleAlaLys...... 223
  GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            815.00
2.890
71.212
2000-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 42.172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396
5
                                                                                                                                                                                                                                                                         248
                                                                                                                                                                                                                                                                                                                                                                             236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-675-784A-12974
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12974, Application US/09675784A GENERAL INFORMATION:
                               SEQ ID NO 12974
                                                   CURRENT APPLICATION NUMBER: US/09/675,784A CURRENT FILING DATE: 2000-09-29 PRIOR APPLICATION NUMBER: 60/156,338 PRIOR FILING DATE: 1999-09-29 NUMBER OF SEQ ID NOS: 13925
                                                                                                                                                                                         APPLICANT: GREENE, JONATHAN R.
TITLE OF INVENTION: ASPERGILLUS FUMIGATUS NUCLEIC ACIDS AND POLYPEPTIDES,
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 2976-4020US1
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HARE, ROBERTA S.
                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1113 TGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1063 AAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 AsnThrIleGlyGlyLysHisGlyIleGlyArgIleAspMetValGluAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        713 TCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTCATGTACCTG 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 uTyrIleGluIleGlyIleGluSerGlyLeuProValAlaLeuAsnGly. 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 663 CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 AspMetTyrMetMetSerValAspProGluAspAlaProAspGlnProGl 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        613 GGTCTCTACACGAAGACCCAGGACCCAAGCCCAAAGCCCCCAACACCCCCTGA 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 euSerHisGluGlyAspLeuLeuGluAspProAlaAsnGluProLysLys 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1163 CCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             813 CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAGCAGGCA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              763 AACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAA 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  427 etGluLysIleThrGluThrThrThrGlySerValThrLeuLysLeuTyr 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 lTyrAlaGlyArgTrpPheAspProLeuArgGluSerMetAspAlaPheM 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         963 GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 GluSerIleGlnValLysAspThrLeuAlaLeuLysTyrAlaGluMetVa 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                913 GAAGTGCGCAAAATCAAACAAGGCCTTGGGCTTGAAATTTGCTGAGCTGGT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460 gGlnAspIleSerSerPheGluGlySerGluIleTyrAsnGlnAlaAspA 477
LENGTH: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 laAlaGlyPheIleArgLeuTyrGlyLeuProMetLys 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hrIleLeuPheAlaAlaValGlnGluLeuGluSerLeuThrLeuAspArg 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....LysAlaLeuSerProAlaThrLeuLeuAlaGluLeu 343
                                                                                                                                                                                                                                                                                              KESSLER, MARCO
NOLLING, JORK
ZENG, QIANDONG
                                                                                                                                                                                                                                                                                                                                                                                      SHIMER JR., GEORGE H.
                                                                                                                                                                                                                                                                                                                                                                                                                SHAW, KAREN J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360
```

```
; ORGANISM: Aspergillus fumigatus US-09-675-784A-12974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block: us-09-675-784A-12974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-09-675-784A-12974 from: 1 to: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-79359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 CCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 IleAspValAlaLysArgGluGlyCysPheAlaValSerHisGlyCysTh 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 GCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 GGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 AAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 CCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAAC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 rGlyLysGlyAsnAspGlnValArgPheGluLeuAlaPheTyrAlaLeuG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 AGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 GTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457 CGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGAT 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 laAsnValGlyGlnGluGluAspPheAspAlaIleArgGluLysAlaLeu 71
                                                                                             657 CCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTG 705
                                                                                                                                         557 TGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCG 606
                                                                                                                                                                                                                                                                                                                               188 eProValThrSerThrLysAlaLysProTrpSerMetAspGluAsnLeuA 205
                                                                                                                                                                                                                                                                                                                                                                           507 TCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCA 556
                                                                                                                                                                                                                                                                                                                                                                                                                       172 ArgPheAlaGlyArgAsnAspLeuLeuSerTyrAlaAlaGluLysGlyIl 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 eGluGlnLeuCysPheProAlaIleAlaCysAsnAlaIleTyrGluAsnV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 LysLeuGlyAlaValLysCysGluIleAlaAspLeuArgArgGluPheIl 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 SerLysGlyLysValCysLeuAlaPheSerGlyGlyLeuAspThrSerVa 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 AGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTG 56
                                                   nProGluAspPheThrValHisPheGluThrGlyIleProValLysLeu 254
                                                                                                                                                                                        CCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACAC 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                759.00
4.059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 60.944
```

seq_documentation_block:

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Ceres Seq. ID 1965190 US-09-708-427-79359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-775-693-1 x US-09-708-427-79359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 655.50
Ratio: 2.953
Percent Similarity: 72.787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-09-708-427-79359 from: 1 to: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATCHIIN VERSION 3.1
SEQ ID NO 79359
LENGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 79359, Application US/09708427 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
EILE REFERENCE: 2750-1243P

EILE REFERENCE: 2750-1243P
144 .....LeuSerProAlaSerLeuLeuAlaGluLeuAsnGluIleGlyGl 158
                                                 727 ACCCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGG 776
                                                                                                      130 lyIleIleAlaGlyValProValSerIle...AsnGlyArgAsp..... 143
                                                                                                                                                           677 AGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATGGCACC 726
                                                                                                                                                                                                             113 tSerIleAlaProGluAsnAlaProSerLysProGluTyrLeuGluIleG 130
                                                                                                                                                                                                                                                               627 GACCCAGGACCCAGCCAAAGCCCCCAACACCCCTGACATTCTCGAGATCG 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: 1..308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                        577 GGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCTACACGAA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                        527 AGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCAGCTACGAGGCT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1..308
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            427 GCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 TCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAGGTCATT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                   97 AspIleLeuGluAspProAlaAsnGluProLysGluAspMetTyrMetMe 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AlaProTrpArgGluTrpAsp......IleThrGlyArgGluAs 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 CTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCCCAGCGGGA 326
                                                                                                                                                                                                                                                                                                                                                                                                                          80 ysSerIleTyrSerArgAspArgAsnLeuTrpHisLeuSerHisGluGly 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 GGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGAACGATCAGG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 alArgPheGluLeuThrPheTyrAlaLeuAsnProGluLeuLysValVal 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 lGlyAlaAspAlaValAlaHisGlyCysThrGlyLysGlyAsnAspGlnV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetAlaArgProValIleAlaLysAlaMetValAspValAlaLysGluVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 44.590
```

```
alignment_scores:
                                                                                                                                                    US-09-708-427-55744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-55744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5574
LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 55744, Appl GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID FILE REFERENCE: 2750-1243P
                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1.309
OTHER INFORMATION: Ceres Seq. ID 1935963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: N. ALEXANDROV et al
                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1..309
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1177 AACATCAATTCCCTC 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1127 GCATGAACGTGCAGGGTGATTATGAGCCAACTGATGCCACCGGGTTCATC 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1077 CATCCTCGGCCGGGAGTCCCCCACTGTCTCTCTACAATGAGGAGCTGGTGA 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1027 GAGCGAGTGGAAGGGAAAGTGCAGGTGTCCGTCCTCAAGGGCCCAGGTGTA 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 ArgLeuTyrGlyLeu 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 erPheGluAsnGlyGluIleTyrAsnGlnAlaAspAlaGluGlyPheIle 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 nValAlaSerArgLysSerProTyrSerLeuTyrArgGluAspIleSerS 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 AlaThrThrGlySerValThrLeuLysLeuTyrLysGlySerValAs 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       977 GGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAG 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   927 CAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTAC 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 rpPheAspProLeuArgClnSerPheAspAlaPheMetGluLysValThr 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 AlaValArgGluLeuGluSerLeuThrLeuAspArgGluThrMetGlnTr 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  877 GCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAAT 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 etLysSerArgGlyValTyrGluThrProGlyGlyThrIleMetAlaAla 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               827 TGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCACCATCCTTTACCAT 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             777 CAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAA 826
                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09708427
639.50
2.947
72.093
```

alignment_block:

Percent Similarity:

Percent Identity: 44.850 Length:

Ratio:

US-09-775-693-1 x US-09-708-427-55744

Align seg 1/1 to: US-09-708-427-55744 from: 1

to: 309

```
1027
1127 GCATGAACGTGCAGGGTGATTATGAGCCAACTGATGCCACCGGGTTCATC 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 CTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCCCAGCGGGA 326
                                                        258 nValAlaSerArgLysSerProTyrSerLeuTyrArgGluAspIleSerS
                                                                                                                                                                                     242 AlaThrThrThrGlySerValThrLeuLysLeuTyrLysGlySerValAs 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 lyIleIleAlaGlyValProValSerIle...AsnGlyArgAsp..... 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 AlaProTrpArgGluTrpAsp......IleThrGlyArgGluAs 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCTACACGAA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGATGGAGTACGCAAAGCAACACGGGATTCCCATCCCGGTCACTCCCA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alArgPheGluLeuThrPheTyrAlaLeuAsnProGluLeuLysValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAGGTCATT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetAlaArgProValIleAlaLysAlaMetValAspValAlaLysGluVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGGAACGATCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysSerIleTyrSerArgAspArgAsnLeuTrpHisLeuSerHisGluGly 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCAGCTACGAGGCT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pAlaIleGluTyrAlaLysLysHisAsnValProValProValSerLysL 80
                                                                                                                      CATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAATGAGGAGCTGGTGA 1126
                                                                                                                                                                                                                                                    GAGCGAGTGGAAGGGAAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTA 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTAC 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAAGTCCCGAGGTATCTACGAGACCCCAGCAGCACCATCCTTTACCAT 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAA 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....LeuSerProAlaSerLeuLeuAlaGluLeuAsnGluIleGlyGl 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATGGCACC 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tSerIleAlaProGluAsnAlaProSerLysProGluTyrLeuGluIleG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACCCAGGACCCAAAGCCCCCAACACCCCTGACATTCTCGAGATCG 676
                                                                                                                                                                                                                                                                                                                  rpPheAspProLeuArgGlnSerPheAspAlaPheMetGluLysValThr 241
                                                                                                                                                                                                                                                                                                                                                                              GGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAG 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaValArgGluLeuGluSerLeuThrLeuAspArgGluThrMetGlnTr 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAAT 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          etLysSerArgGlyValTyrGluThrProGlyGlyThrIleMetAlaAla 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGG 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspIleLeuGluAspProAlaAsnGluProLysGluAspMetTyrMetMe 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50
```

erPheGluAsnGlyGluIleTyr.AsnGln***ThrProArgGlySerSe

291

```
NAME/KEY: misc_feature
LCATION: 1..283
COTHER INFORMATION: Ceres Seq.
US-09-708-427-11259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-775-693-1 x US-09-708-427-11259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-11259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P CURRENT SPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: PATENTIAL OF SEQ ID NOS: 85364 SOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11259, Application US/09708427 GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-09-708-427-11259 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 1..283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1177 A 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 r 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 TCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCAGATAAAGGTCATT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 GGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGAACGATCAGG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 CTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCCCAGCGGGA 326
                                                                                                                                                                                                                                                                                         577 GGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCTACACGAA 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   527 AGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCAGCTACGAGGCT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        477 CCTGATGGAGTACGCAAAGCAACACGGGATTCCCATCCCGGTCACTCCCA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  427 GCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 pAlaIleGluTyrAlaLysLysHisAsnValProValProValThrLysL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 AlaProTrpArgGluTrpGlu......IleGlnGlyArgGluAs
88 tSerValAspProGluAspAlaProAspGlnProGluTyrIleGluIleG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :::|||||||| |||||:::
1 MetAlaArgProValIleAlaLys...........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                               GACCCAGGACCCAGCCAAAGCCCCCAACACCCCTGACATTCTCGAGATCG 676
                                                                                                                                                                                         :::||||||:::||| ||||:::
AspLeuLeuGluAspProAlaAsnGluProLysLysAspMetTyrMetMe 88
                                                                                                                                                                                                                                                                                                                                                                                   ysSerIleTyrSerArgAspArgAsnLeuTrpHisLeuSerHisGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       598.00
2.875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 40.260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID 1822816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    œ
                                                                                                                                                                                                                                                                                                                                                                                                  71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38
```

```
; OTHER INFORMATION: MAP TO ACO04616.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.83
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: SWISSPROT HIT: P00966, EVALUE 6.00e-48
US-10-029-386-32991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
Sequence 32991, Application US/10029386
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FITLE REFERENCE: AEOMICA-X-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-029-386-32991
                                                                                                                                                                                                                                                                                                                          SEQ ID NO 32991
LENGTH: 138
                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1177 AACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1077 CATCCTCGGCCGGAGTCCCCACTGTCTCTACAATGAGGAGCTGGTGA 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 erPheGluGlySerGluIleTyrAsnGlnAlaAspAlaAlaGlyPheIle 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 GluThrThrThrGlySerValThrLeuLysLeuTyrLysGlySerValSe 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 rpPheAspProLeuArgGluSerMetAspAlaPheMetGluLysIleThr 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 lLysAspThrLeuAlaLeuLysTyrAlaGluMetValTyrAlaGlyArgT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               927 CAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTTAC 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           877 GCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCCAAAAT 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 yLysHisGlyIleGlyArgIleAspMetValGluAsnArgLeuValGlyM 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 LysAlaLeuSerProAlaThrLeuLeuAlaGluLeuAsnThrIleGlyGl 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 lyIleGluSerGlyLeuProValAlaLeuAsnGly.................. 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                677 AGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATGGCACC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      727 ACCCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGG 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCATGAACGTGCAGGGTGATTATGAGCCAACTGATGCCACCGGGTTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt rValThrGlyArgGlnSerProAsnSerLeuTyrArgGlnAspIleSerS}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGCGAGTGGAAGGGAAAGTGCAGGTGTCCGTCCTCAAGGGCCCAGGTGTA 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAG 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgLeuTyrGlyLeuProMetLys 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaValGlnGluLeuGluSerLeuThrLeuAspArgGluSerIleGlnVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAA 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183
```

```
alignment_block:
US-09-775-693-1 x US-10-029-386-32991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-10-029-386-32991 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 477.00
Ratio: 4.500
Percent Similarity: 96.364
                                                         101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG
                                                                                                                                                                                                         151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                             78
                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                    28 ValSerSerLysGlySerMetValLeuAlaHisSerGlyGlyLeuAspTh
                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC
               AAACAAGTGGAAAATCGCCCAGCGGGAGGGG 330
LysGlnValGluIleThrGlnGlnGluGly 137
                                                                                        AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                       {\tt yrLeuAlaLysIleSerGlnLysGluAspPheGluAspAspArgLysLys}
                                                                                                                                                                                        AlaTrpLysLeuGlyAlaLysLysValPheIleAspAspValSerArgAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 110
Gaps: 0
Percent Identity: 84.545
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ţo:
                                                             127
                                                                                                                                                                                          94
                                                                                                                                                                                                                                                         77
                                                                                                                                                                                                                                                                                         150
                                                                                                                                                                                                                                                                                                                                                                                      44
```

				,
				310
	,			